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## OM protein - protein search, using sw model

Run on: May 11, 2004, 16:20:26 ; Search time 23 Seconds

(without alignments)  
693.584 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574  
Sequence: 1 HASAHASGRORQLHSASTQI.....SSFPALSWALLPISPYMLK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1574	100.0	309	4	US-09-404-879A-392	Sequence 392, App *
2	1431	90.9	282	4	US-09-404-879A-393	Sequence 393, App *
3	247	15.7	316	4	US-09-910-174B-24	Sequence 24, Appl
4	247	15.7	316	4	US-09-620-461-24	Sequence 24, Appl
5	246	15.6	441	4	US-09-651-200-4	Sequence 4, Appl
6	246	15.6	534	4	US-09-651-200-6	Sequence 6, Appl
7	246	15.6	534	4	US-09-651-200-24	Sequence 24, Appl
8	245	15.6	340	4	US-09-651-200-2	Sequence 2, Appl
9	238.5	15.2	315	4	US-09-910-174B-28	Sequence 28, Appl
10	238.5	15.2	315	4	US-09-620-461-28	Sequence 28, Appl
11	223	14.2	513	4	US-09-910-174B-18	Sequence 18, Appl
12	223	14.2	513	4	US-09-620-461-18	Sequence 18, Appl
13	217.5	13.8	540	2	US-08-724-394A-4	Sequence 4, Appl
14	215.5	13.7	731	4	US-09-910-174B-15	Sequence 15, Appl
15	215.5	13.7	731	4	US-09-620-461-15	Sequence 15, Appl
16	213.5	13.6	584	4	US-09-620-461-16	Sequence 16, Appl
17	213.5	13.6	584	4	US-09-620-461-16	Sequence 16, Appl
18	212.5	13.4	610	2	US-08-724-394A-5	Sequence 5, Appl
19	211.5	13.4	526	4	US-09-910-174B-9	Sequence 9, Appl
20	211.5	13.4	526	4	US-09-620-461-9	Sequence 9, Appl
21	211.5	13.4	589	2	US-08-724-394A-1	Sequence 1, Appl
22	207.5	13.2	319	4	US-09-910-174B-12	Sequence 12, Appl
23	207.5	13.2	319	4	US-09-620-461-12	Sequence 12, Appl
24	207.5	13.2	342	2	US-08-724-394A-6	Sequence 6, Appl
25	207.5	13.2	357	4	US-09-910-174B-14	Sequence 14, Appl
26	207.5	13.2	357	4	US-09-620-461-14	Sequence 14, Appl
27	204	13.0	290	4	US-09-910-174B-19	Sequence 19, Appl

28	204	13.0	290	4	US-09-620-461-19	Sequence 19, Appl
29	204	13.0	350	4	US-09-651-200-25	Sequence 25, Appl
30	204	13.0	350	4	US-09-910-174B-17	Sequence 17, Appl
31	204	13.0	350	4	US-09-620-461-17	Sequence 17, Appl
32	199.5	12.7	290	4	US-09-910-174B-32	Sequence 32, Appl
33	196	12.5	296	4	US-09-667-135-36	Sequence 36, Appl
34	193	12.3	527	4	US-09-910-174B-10	Sequence 10, Appl
35	193	12.3	527	4	US-09-620-461-10	Sequence 10, Appl
36	192	12.2	329	4	US-09-651-200-18	Sequence 18, Appl
37	192	12.2	329	4	US-09-303-040-6	Sequence 6, Appl
38	188.5	12.0	290	4	US-09-910-174B-8	Sequence 8, Appl
39	188.5	12.0	290	4	US-09-620-461-8	Sequence 8, Appl
40	186	11.8	529	4	US-09-910-174B-13	Sequence 13, Appl
41	186	11.8	529	4	US-09-620-461-13	Sequence 13, Appl
42	186	11.8	581	2	US-08-724-394A-2	Sequence 2, Appl
43	183	11.6	523	4	US-09-910-174B-11	Sequence 11, Appl
44	183	11.6	523	4	US-09-620-461-11	Sequence 11, Appl
45	183	11.6	581	2	US-08-724-394A-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-404-879A-392 \*  
; Sequence 392, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.462C2  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 393  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 392  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-404-879A-392

Query Match	100.0%	Score 1574	DB 4	Length 309
Best Local Similarity	100.0%	Pred. No. 1.3e-153		
Matches 309	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	HASAHASGRORQLHSASTQIRWEPSPAMASIGQILFMSIISIIIIAGAILIIGFISG	60	
DB	1	HASAHASGRORQLHSASTQIRWEPSPAMASIGQILFMSIISIIIIAGAILIIGFISG	60	
QY	61	RHSITVTYASAGNIGEDGILSTFEPDIKSDIVIQMLKEGVLGVHFEKKGKDELSQ	120	
DB	61	RHSITVTYASAGNIGEDGILSTFEPDIKSDIVIQMLKEGVLGVHFEKKGKDELSQ	120	
QY	121	DEMEFGRIVADQYIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP	180	
DB	121	DEMEFGRIVADQYIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP	180	
QY	181	EENVVYNASSETLRCEAPRFPPOPTVWVASQVDOGANFSEVNTSFEINSEVTKVVS	240	
DB	181	EENVVYNASSETLRCEAPRFPPOPTVWVASQVDOGANFSEVNTSFEINSEVTKVVS	240	
QY	241	LYNVTINNTYSCMTENDIKATGDIKVTSEIRRSRSHQLNSKASLCVSSFPALISWALL	300	
DB	241	LYNVTINNTYSCMTENDIKATGDIKVTSEIRRSRSHQLNSKASLCVSSFPALISWALL	300	
QY	301	PLSPYIMLK 309		
DB	301	PLSPYIMLK 309		

RESULT 2  
US-09-404-879A-393  
; Sequence 393, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C2  
; CURRENT APPLICATION NUMBER: US/09/404, 879A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 393  
; SOFTWARE: FastSeq for Windows Version 3.10  
; SEQ ID NO 393  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-404-879A-393

Query Match 90.9%; Score 1431; DB 4; Length 282;  
Best Local Similarity 100.0%; Pred. No. 5.8e-139;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWISIIIIIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDGILSCPEP 87  
DB 1 MASLGQILFWISIIIIIIIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDGILSCPEP 60  
QY 88 DIKLSDIVIOWLKEGVLGVHFEKGEKDELSEODEMFRGRTAVFADQVIVGNASLRKXV 147  
DB 61 DIKLSDIVIOWLKEGVLGVHFEKGEKDELSEODEMFRGRTAVFADQVIVGNASLRKXV 120  
QY 148 QLTDAGYTKCYIITTSKKGANLLEYKTGAFSMEPVVVDYVASSETLRCAAPRFPQPTVY 207  
DB 121 QLTDAGYTKCYIITTSKKGANLLEYKTGAFSMEPVVVDYVASSETLRCAAPRFPQPTVY 180  
QY 208 WASQVDGAFSEVSNSTSEFENSEVTMTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267  
DB 181 WASQVDGAFSEVSNSTSEFENSEVTMTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 240  
QY 268 TSEIKRSHLOLNSKASLCVSSFFAISWALLPLSPYLMK 309  
DB 241 TSEIKRSHLOLNSKASLCVSSFFAISWALLPLSPYLMK 282

RESULT 3  
US-09-910-174B-24  
; Sequence 24, Application US/09910174B  
; Patent No. 6630575  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Frazer, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
; TITLE OF INVENTION: Family and Uses Thereof  
; FILE REFERENCE: 35800/236924  
; CURRENT APPLICATION NUMBER: US/09/910, 174B  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 09/620, 461  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-910-174B-24

Query Match 15.7%; Score 247; DB 4; Length 316;  
Best Local Similarity 28.5%; Pred. No. 5.3e-17;  
Matches 74; Conservative 46; Mismatches 106; Indels 34; Gaps 10;

QY 20 IRWESPAMASLGQILFWISIIIIIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDG 79  
DB 2 LRRRSPGMSG-----VHVGAAALGALMFCLTGALVEQVPEDEPVVALVGTDA 46  
QY 80 ILSCPE--EPDIKLSDIVIOWLKEGVLGVHFEKGEKDELSEODEMFRGRTAVFADQVIV 137  
DB 47 TLCCSFSPBEPFSLAQLNLIWQLTDTKQLVHSPABEQD---QGSAYANRTALFPDLAAQ 102  
QY 138 GNASLRKXVQLTDAGYTKCYIITTSKKGANLLEYKTGA-FSMEPVVVDYV-----ASSE 191  
DB 103 GNASLRKXVQLTDAGYTKCYIITTSKKGANLLEYKTGA-FSMEPVVVDYV-----ASSE 161  
QY 192 TLRCAPRMPFPQPTVWASQVDGAFSEVSNSTSEFENSEVTMTKVSVLYNVT-INNTY 250  
DB 162 TITCSSYRGVPEAEVFW--QDGGGVPLTGNVTS-QMANEGGLFDVHSLRVVLGANGTY 218  
QY 251 SCMIENDIAK--ATGDIKVT 268  
DB 219 SCLVRNPVTLQDDAHGSVTIT 238

RESULT 4  
US-09-620-461-24  
; Sequence 24, Application US/09620461  
; Patent No. 6635750  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Frazer, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
; TITLE OF INVENTION: Family and Uses Thereof  
; FILE REFERENCE: 5800-149  
; CURRENT APPLICATION NUMBER: US/09/620, 461  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.10  
; SEQ ID NO 24  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-620-461-24

Query Match 15.7%; Score 247; DB 4; Length 316;  
Best Local Similarity 28.5%; Pred. No. 5.3e-17;  
Matches 74; Conservative 46; Mismatches 106; Indels 34; Gaps 10;

QY 20 IRWESPAMASLGQILFWISIIIIIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDG 79  
DB 2 LRRRSPGMSG-----VHVGAAALGALMFCLTGALVEQVPEDEPVVALVGTDA 46  
QY 80 ILSCPE--EPDIKLSDIVIOWLKEGVLGVHFEKGEKDELSEODEMFRGRTAVFADQVIV 137  
DB 47 TLCCSFSPBEPFSLAQLNLIWQLTDTKQLVHSPABEQD---QGSAYANRTALFPDLAAQ 102  
QY 138 GNASLRKXVQLTDAGYTKCYIITTSKKGANLLEYKTGA-FSMEPVVVDYV-----ASSE 191  
DB 103 GNASLRKXVQLTDAGYTKCYIITTSKKGANLLEYKTGA-FSMEPVVVDYV-----ASSE 161  
QY 192 TLRCAPRMPFPQPTVWASQVDGAFSEVSNSTSEFENSEVTMTKVSVLYNVT-INNTY 250  
DB 162 TITCSSYRGVPEAEVFW--QDGGGVPLTGNVTS-QMANEGGLFDVHSLRVVLGANGTY 218  
QY 251 SCMIENDIAK--ATGDIKVT 268  
DB 219 SCLVRNPVTLQDDAHGSVTIT 238

RESULT 5  
US-09-651-200-4  
; Sequence 4, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al

DR N-PSDB; AA265059.  
XX Membrane-bound proteins and related nucleotide sequences.  
XX  
XX  
XX Claim 12; Fig 208; 822pp; English.  
XX  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
XX Sequence 282 AA; **WC99463088-A2**

Query Match 90.9%; Score 1431; DB 3; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIISIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDGILSCFEP 87  
DB 1 MASLGQILFWSIIISIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDGILSCFEP 60  
QY 88 DIKLSDIVIOWLKEGVLGVHEFEKGEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 147  
DB 61 DIKLSDIVIOWLKEGVLGVHEFEKGEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 120  
QY 148 QLTDACTYKCYIITTSKGGKGNANLEKXTGAFSMPENVVDYNASSETLRCEAPRFPQPTV 207  
DB 121 QLTDACTYKCYIITTSKGGKGNANLEKXTGAFSMPENVVDYNASSETLRCEAPRFPQPTV 180  
QY 208 WASQVDGANESEVNTSFEINSENVMTKRVSVLYNTINNTYSCMIENDIAKATGDIKV 267  
DB 181 WASQVDGANESEVNTSFEINSENVMTKRVSVLYNTINNTYSCMIENDIAKATGDIKV 240  
QY 268 TESEIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYIMLK 309  
DB 241 TESEIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYIMLK 282

## RESULT 6

AAB12557  
ID AAB12557\*standard; protein; 282 AA.

XX AAB12557;  
XX  
XX 07-NOV-2000 (first entry)  
XX  
XX Human ovarian carcinoma antigen OBE protein SEQ ID NO:393.  
XX  
XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;  
XX tumour antigen; identification; cytostatic; gene therapy; vaccine.  
XX  
XX Homo sapiens.  
XX  
XX WO200036107-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 17-DEC-1999; 99WO-US030270.  
XX  
XX 17-DEC-1998; 98US-00215681.  
XX 17-DEC-1998; 98US-00216003.  
XX 23-JUN-1999; 99US-00338933.  
XX 24-SEP-1999; 99US-00404879.

XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Mitcham JL, King GE, Algate PA, Frudakis TN;  
XX  
XX WPI; 2000-431589/37.  
XX  
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid  
XX encoding it, useful for the diagnosis, prevention and treatment of  
XX cancer, preferably ovarian cancer.  
XX  
XX Example 2; Page 207; 299pp; English.  
XX  
XX The present invention describes an isolated polypeptide comprising an  
XX immunogenic portion of an ovarian carcinoma protein (or its variants).  
XX Ovarian carcinoma proteins, and polynucleotides encoding them, have  
XX cytostatic activity and can be used in gene therapy and vaccines. Ovarian  
XX carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful  
XX for the prevention, diagnosis and treatment of cancer, preferably ovarian  
XX cancer. AA69691 to AA70077 and AAB12552 to AAB12557 represent human  
XX ovarian carcinoma polynucleotides and proteins used in the  
XX exemplification of the present invention

Sequence 282 AA;  
Query Match 90.9%; Score 1431; DB 3; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIISIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDGILSCFEP 87  
DB 1 MASLGQILFWSIIISIIIIAGALALIIIGFISGRHSITVTTVASAGNIGEDGILSCFEP 60  
QY 88 DIKLSDIVIOWLKEGVLGVHEFEKGEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 147  
DB 61 DIKLSDIVIOWLKEGVLGVHEFEKGEKDELSEODEMFRGRTAVFADQYIVGNASLRKNV 120  
QY 148 QLTDACTYKCYIITTSKGGKGNANLEKXTGAFSMPENVVDYNASSETLRCEAPRFPQPTV 207  
DB 121 QLTDACTYKCYIITTSKGGKGNANLEKXTGAFSMPENVVDYNASSETLRCEAPRFPQPTV 180  
QY 208 WASQVDGANESEVNTSFEINSENVMTKRVSVLYNTINNTYSCMIENDIAKATGDIKV 267  
DB 181 WASQVDGANESEVNTSFEINSENVMTKRVSVLYNTINNTYSCMIENDIAKATGDIKV 240  
QY 268 TESEIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYIMLK 309  
DB 241 TESEIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYIMLK 282

## RESULT 7

AAU29132  
ID AAU29132 standard; protein; 282 AA.

XX AAU29132;  
XX  
XX 18-DEC-2001 (first entry)  
XX  
XX Human PRO polypeptide sequence #109.  
XX  
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX  
XX Homo sapiens.  
XX  
XX WO200168848-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 28-FEB-2001; 2001WO-US006520.  
XX

01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 06-MAR-2000; 2000US-0186368P.  
PR 14-MAR-2000; 2000US-0189320P.  
PR 14-MAR-2000; 2000US-0189328P.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 21-MAR-2000; 2000US-0190828P.  
PR 21-MAR-2000; 2000US-0191007P.  
PR 21-MAR-2000; 2000US-0191048P.  
PR 21-MAR-2000; 2000US-0191314P.  
PR 28-MAR-2000; 2000US-0192655P.  
PR 29-MAR-2000; 2000US-0193032P.  
PR 29-MAR-2000; 2000US-0193053P.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 04-APR-2000; 2000US-0194449P.  
PR 04-APR-2000; 2000US-0194647P.  
PR 11-APR-2000; 2000US-0195975P.  
PR 11-APR-2000; 2000US-0196000P.  
PR 11-APR-2000; 2000US-0196187P.  
PR 11-APR-2000; 2000US-0196690P.  
PR 18-APR-2000; 2000US-0196820P.  
PR 18-APR-2000; 2000US-0198121P.  
PR 18-APR-2000; 2000US-0198585P.  
PR 25-APR-2000; 2000US-0199397P.  
PR 25-APR-2000; 2000US-0199550P.  
PR 25-APR-2000; 2000US-0199654P.  
PR 03-MAY-2000; 2000US-0201516P.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
XX  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI; 2001-602746/68.  
DR N-PSDB; AAS46033.  
XX  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.  
XX  
XX Claim 11; Fig 218; 774pp; English.  
PS  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
XX  
SQ Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 4; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 MASLQILFMSIISIIIIAGALALIGFGISGRHSITVTVAASAGNIGEDGILSCFEP 87  
DB 1 MASLQILFMSIISIIIIAGALALIGFGISGRHSITVTVAASAGNIGEDGILSCFEP 60  
QY 88 DIKLSDIVIQLKRGVLGLVHEFEKDELSEDEMRGRTRAVFADQYIVGNASLRKNV 147  
DB 61 DIKLSDIVIQLKRGVLGLVHEFEKDELSEDEMRGRTRAVFADQYIVGNASLRKNV 120  
QY 148 QLTDACTKYCIITISKGNANLEYKTGAFSMEVDVNDYNASSETLRCEAPRFPQPTVV 207  
DB 121 QLTDACTKYCIITISKGNANLEYKTGAFSMEVDVNDYNASSETLRCEAPRFPQPTVV 180  
QY 208 WASQVDQANFSEVSNTSEPLNSEVTMKVSVLYNVTINNTVSCMTENDIAKATGDIKV 267  
DB 181 WASQVDQANFSEVSNTSEPLNSEVTMKVSVLYNVTINNTVSCMTENDIAKATGDIKV 240  
QY 268 TSEIKRRSHLQLNSKASLCVSSFFAISWALLPLSPYLMX 309  
DB 241 TSEIKRRSHLQLNSKASLCVSSFFAISWALLPLSPYLMX 282

RESULT 8  
AAB87555  
ID AAB87555 standard; protein; 282 AA.  
XX  
XX AAB87555;  
AC  
XX 15-MAY-2001 (first entry)  
DT  
XX Human PRO1291.  
DE  
XX Human; PRO protein; mapping.  
KW  
XX Homo sapiens.  
OS  
XX WO200116318-A2.  
PN  
XX 08-MAR-2001.  
PD  
XX 24-AUG-2000; 2000WO-US023328.  
PF  
XX  
XX 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021090.  
PR 07-DEC-1999; 99US-0169495P.  
PR 09-DEC-1999; 99US-0170262P.  
PR 11-JAN-2000; 2000US-0175481P.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 21-MAR-2000; 2000US-0191007P.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 25-APR-2000; 2000US-0199397P.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 05-JUN-2000; 2000US-0209832P.  
XX  
XX (GETH ) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX  
XX WPI; 2001-183260/18.  
DR N-PSDB; AAF92087.  
XX  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular  
PT biology, including use as hybridization probes, and in chromosome and  
PT gene mapping.  
XX



SQ Sequence 309 AA:

Query Match 100.0%; Score 1574; DB 3; Length 309;  
Best Local Similarity 100.0%; Pred. No. 6.7e-130;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 HASAHASGRQRLHASTQIRWEPSPAMASLGQILFWSIISIIIIAGAILIIGFISG 60
DB 1 HASAHASGRQRLHASTQIRWEPSPAMASLGQILFWSIISIIIIAGAILIIGFISG 60
QY 61 RHSITVTVAAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVLGVHEFEKXDELSEQ 120
DB 61 RHSITVTVAAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVLGVHEFEKXDELSEQ 120
QY 121 DEMFRGRTAVFADQIVGNASLRKKNVQLTDAGTYKCYIITSKKGANALEYKTGFSP 180
DB 121 DEMFRGRTAVFADQIVGNASLRKKNVQLTDAGTYKCYIITSKKGANALEYKTGFSP 180
QY 181 EVNVVDYNASSETLRCEAPRFPOPTVWASQVDQANFSEVSNTSFELNSENVMTKVS 240
DB 181 EVNVVDYNASSETLRCEAPRFPOPTVWASQVDQANFSEVSNTSFELNSENVMTKVS 240
QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLNSKASLCVSSFFAISW 300
DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLNSKASLCVSSFFAISW 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309
```

RESULT 2

AAB99205 AAB99205 standard; protein; 309 AA.

```
XX AC AAB99205;
XX DT 04-SEP-2001 (first entry)
XX DE Human ovarian tumour-derived antigen O8E #2.
XX KM Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
XX OS Homo sapiens.
XX PN WO200140269-A2.
XX PD 07-JUN-2001.
XX PF 29-NOV-2000; 2000WO-US032520.
XX PR 30-NOV-1999; 99US-00451651.
XX PR 22-FEB-2000; 2000US-00510662.
XX PR 10-MAR-2000; 2000US-00523586.
XX PR 07-APR-2000; 2000US-00545068.
XX PR 15-MAY-2000; 2000US-00571025.
XX PA (CORI-) CORIXA CORP.
XX PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX DR N-PSDB; AAH55681.
XX PT Breast tumor polypeptides and the nucleic acids that encode them, useful
XX PS for the prevention, diagnosis and treatment of breast cancer.
XX PS Example 3; Page 191-192; 221pp; English.
```

CC The present invention relates to human breast tumour protein coding  
CC sequences (see AAH55479-AAH5513, AAH5517-AAH55679 and AAH55682-  
CC AAH55762). The breast tumour protein DNA sequences may be used in the

CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the breast tumour protein e.g. breast cancer.  
CC The present sequence is a human ovarian tumour-derived antigen, which was  
CC used in an example from the present invention

SQ Sequence 309 AA:

Query Match 100.0%; Score 1574; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 6.7e-130;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 HASAHASGRQRLHASTQIRWEPSPAMASLGQILFWSIISIIIIAGAILIIGFISG 60
DB 1 HASAHASGRQRLHASTQIRWEPSPAMASLGQILFWSIISIIIIAGAILIIGFISG 60
QY 61 RHSITVTVAAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVLGVHEFEKXDELSEQ 120
DB 61 RHSITVTVAAGNIGEDGILSCTFEEDIKLSDIVIQWLKEGVLGVHEFEKXDELSEQ 120
QY 121 DEMFRGRTAVFADQIVGNASLRKKNVQLTDAGTYKCYIITSKKGANALEYKTGFSP 180
DB 121 DEMFRGRTAVFADQIVGNASLRKKNVQLTDAGTYKCYIITSKKGANALEYKTGFSP 180
QY 181 EVNVVDYNASSETLRCEAPRFPOPTVWASQVDQANFSEVSNTSFELNSENVMTKVS 240
DB 181 EVNVVDYNASSETLRCEAPRFPOPTVWASQVDQANFSEVSNTSFELNSENVMTKVS 240
QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLNSKASLCVSSFFAISW 300
DB 241 LYNVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLNSKASLCVSSFFAISW 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309
```

RESULT 3

ABP30900 ABP30900 standard; protein; 309 AA.

```
XX AC ABP30900;
XX DT 02-JUL-2002 (first entry)
XX DE O8E protein #1.
XX KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
XX OS Homo sapiens.
XX PN WO200206317-A2.
XX PD 24-JAN-2002.
XX PF 17-JUL-2001; 2001WO-US022635.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
XX PR 20-SEP-2000; 2000US-00667857.
XX PR 04-APR-2001; 2001US-00827271.
XX PR 18-JUN-2001; 2001US-00884441.
XX PA (CORI-) CORIXA CORP.
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX DR N-PSDB; ABN72971.
XX PS WPI: 2002-164781/21.
```

CC Polypeptides comprising an immunogenic portion of an ovarian carcinoma  
CC protein or its variants, useful for stimulating an immune response in a  
CC patient and treating ovarian cancer.

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## OM protein - protein search, using 'sw model

Run on: May 11, 2004, 16:00:15 ; Search time 59 Seconds

(without alignments)  
1479.783 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574  
Sequence: 1 HASAHASGRQRQLHASASTQL.....SSFFAISMALLPLSPYIMLK 309Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1574	100.0	309	4	AAAB12556 Human ova
2	1574	100.0	309	3	AAAB99205 Human ova
3	1574	100.0	309	5	ABP30900 OBE prote
4	1574	100.0	309	7	ADA08545 Human ova
5	1431	90.9	282	3	AAAY66719 Membrane-
6	1431	90.9	282	3	AAAB12557 Human ova
7	1431	90.9	282	4	AAU29132 Human PRO
8	1431	90.9	282	4	AAAB87555 Human PRO
9	1431	90.9	282	4	AAAB99204 Human ova
10	1431	90.9	282	4	AAAB65242 Human PRO
11	1431	90.9	282	5	AAAE0311 Human B7-
12	1431	90.9	282	5	ABG96445 Human ova
13	1431	90.9	282	5	AAU77766 Tumour as
14	1431	90.9	282	5	ABG95880 Human sec
15	1431	90.9	282	5	AAU76536 Tumour-as
16	1431	90.9	282	5	ABP30901 OBE prote
17	1431	90.9	282	5	ABP76274 Breast BS
18	1431	90.9	282	5	AAE18336 Human B7-
19	1431	90.9	282	5	ABBO9879 Amino aci
20	1431	90.9	282	6	AAE19013 Human B7-
21	1431	90.9	282	6	ABU58508 Human PRO
22	1431	90.9	282	6	ABU88056 Novel hum
23	1431	90.9	282	6	ABU84371 Human sec
24	1431	90.9	282	6	ABR66245 Human sec
25	1431	90.9	282	6	ABR65635 Human sec

26	1431	90.9	282	6	ABU99575 Human sec
27	1431	90.9	282	6	ABU58057 Human PRO
28	1431	90.9	282	6	ABU59135 Novel hum
29	1431	90.9	282	6	ABU82647 Human sec
30	1431	90.9	282	6	ABU82814 Human PRO
31	1431	90.9	282	6	ABU89935 Novel hum
32	1431	90.9	282	6	ABR68184 Human sec
33	1431	90.9	282	6	ABU60566 Human sec
34	1431	90.9	282	6	ABU96237 Novel hum
35	1431	90.9	282	6	ABU92668 Human sec
36	1431	90.9	282	6	ABO08745 Human sec
37	1431	90.9	282	6	ABO02797 Human sec
38	1431	90.9	282	6	ABR74951 Human sec
39	1431	90.9	282	6	ABR94713 Human sec
40	1431	90.9	282	6	ABU13948 Human PRO
41	1431	90.9	282	6	ABU85686 Human PRO
42	1431	90.9	282	6	ABU98846 Novel hum
43	1431	90.9	282	6	ABU98061 Novel hum
44	1431	90.9	282	6	ABU91767 Novel hum
45	1431	90.9	282	6	ABU89460 Human PRO

## ALIGNMENTS

RESULT 1	
AAAB12556	
ID	AAAB12556 standard; protein; 309 AA.
XX	
AC	AAAB12556;
XX	
DT	07-NOV-2000 (first entry)
XX	
DE	Human ovarian carcinoma antigen OBE protein SEQ ID NO:392.
XX	
KW	Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW	tumour antigen; identification; cytostatic; gene therapy; vaccine.
XX	
OS	Homo sapiens.
XX	
PN	WO200036107-A2.
XX	
PD	22-JUN-2000.
XX	
PF	17-DEC-1999; 99WO-US030270.
XX	
PR	17-DEC-1998; 98US-00215681.
PR	17-DEC-1998; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Mitcham JL, King GE, Algate PA, Frudakis TN;
XX	WPI; 2000-431589/37.
DR	
XX	
PT	Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT	encoding it, useful for the diagnosis, prevention and treatment of
PT	cancer, preferably ovarian cancer.
XX	
PS	Example 2; Page 205-206; 299pp; English.
XX	
CC	The present invention describes an isolated polypeptide comprising an
CC	immunogenic portion of an ovarian carcinoma protein (or its variants).
CC	Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC	cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC	carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC	for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC	cancer. AA69691 to AA70077 and AA12552 to AA12557 represent human
CC	ovarian carcinoma polynucleotides and proteins used in the
CC	exemplification of the present invention
XX	

XX Example 2; Page 320-321; 408bp; English.  
XX  
PS  
CC This invention relates to polypeptides comprising an immunogenic portion  
CC of an ovarian carcinoma protein which acts as an immunostimulant and is  
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations and antigen presenting cells that express  
CC the polypeptides are useful for stimulating an immune response in a  
CC patient and treating ovarian cancer. This sequence represents protein  
CC related to the invention  
XX  
SQ Sequence 309 AA;  
Query Match 100.0%; Score 1574; DB 5; Length 309;  
Best Local Similarity 100.0%; Pred. No. 6.7e-130;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HASAHASGRQRLHSASTQIRWEPSPAMASIGQILFWSTISIIIIILAGAILIIGFGISG 60  
DB 1 HASAHASGRQRLHSASTQIRWEPSPAMASIGQILFWSTISIIIIILAGAILIIGFGISG 60  
QY 61 RHSITVTVASAGNIGEDGILSCTFEPDILKLSDIVIQWLKEGVLGLVHEKKEGDELSEQ 120  
DB 61 RHSITVTVASAGNIGEDGILSCTFEPDILKLSDIVIQWLKEGVLGLVHEKKEGDELSEQ 120  
QY 121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180  
DB 121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180  
QY 181 EVAVDYNASSETLRCEAPRWFPQPTVWASQVDGANGFSEVSNISFELNSENVTMKVSV 240  
DB 181 EVAVDYNASSETLRCEAPRWFPQPTVWASQVDGANGFSEVSNISFELNSENVTMKVSV 240  
QY 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHQLNLNSKASLVCVSSFALISWALL 300  
DB 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHQLNLNSKASLVCVSSFALISWALL 300  
QY 301 PLSPLYMLK 309  
DB 301 PLSPLYMLK 309  
RESULT 4  
ADA08545  
ID ADA08545 standard; protein; 309 AA.  
XX  
AC ADA08545;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human ovarian carcinoma polynucleotide O8E protein #1.  
XX  
KM human; gene therapy; ovarian cancer; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003091580-A1.  
XX  
PD 15-MAY-2003.  
XX  
PF 17-JUL-2001; 2001US-00907969.  
XX  
PR 18-JUN-2001; 2001US-00884441.  
XX  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.

PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
XX  
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,  
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;  
XX  
DR WPI; 2003-532352/50.  
XX  
XX  
PT New isolated 0772P polypeptides and polynucleotides, useful in gene  
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 392; 371bp; English.  
XX  
CC The invention relates to an isolated 0772P polypeptide, which has the  
CC structure fully defined in the specification. The composition containing  
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells  
CC or antigen presenting cells are useful for stimulating an immune response  
CC and treating ovarian cancer. Detecting the presence of the  
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian  
CC carcinoma cDNAs and protein cDNAs were identified using microarray  
CC technology. The present sequence represents a human ovarian carcinoma  
CC antigen.  
XX  
SQ Sequence 309 AA;  
Query Match 100.0%; Score 1574; DB 7; Length 309;  
Best Local Similarity 100.0%; Pred. No. 6.7e-130;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HASAHASGRQRLHSASTQIRWEPSPAMASIGQILFWSTISIIIIILAGAILIIGFGISG 60  
DB 1 HASAHASGRQRLHSASTQIRWEPSPAMASIGQILFWSTISIIIIILAGAILIIGFGISG 60  
QY 61 RHSITVTVASAGNIGEDGILSCTFEPDILKLSDIVIQWLKEGVLGLVHEKKEGDELSEQ 120  
DB 61 RHSITVTVASAGNIGEDGILSCTFEPDILKLSDIVIQWLKEGVLGLVHEKKEGDELSEQ 120  
QY 121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180  
DB 121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180  
QY 181 EVAVDYNASSETLRCEAPRWFPQPTVWASQVDGANGFSEVSNISFELNSENVTMKVSV 240  
DB 181 EVAVDYNASSETLRCEAPRWFPQPTVWASQVDGANGFSEVSNISFELNSENVTMKVSV 240  
QY 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHQLNLNSKASLVCVSSFALISWALL 300  
DB 241 LYNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHQLNLNSKASLVCVSSFALISWALL 300  
QY 301 PLSPLYMLK 309  
DB 301 PLSPLYMLK 309  
RESULT 5  
AAY66719  
ID AAY66719 standard; protein; 282 AA.  
XX  
AC AAY66719;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1291.  
XX  
DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KM pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO9963088-A2.  
XX  
PD 09-DEC-1999.

XX 02-JUN-1999; 99WO-US012252.  
PF  
XX  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-008759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088126P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088730P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089090P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089947P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090445P.  
PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090472P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090538P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 24-JUN-1998; 98US-0090557P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090691P.

PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091358P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
PR 10-AUG-1998; 98US-0095929P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 11-AUG-1998; 98US-0096143P.  
PR 11-AUG-1998; 98US-0096146P.  
PR 12-AUG-1998; 98US-0096329P.  
PR 12-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096768P.  
PR 17-AUG-1998; 98US-0096773P.  
PR 17-AUG-1998; 98US-0096791P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096894P.  
PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0096960P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-009761P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.

(GETH ) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J;  
XX  
DR WPI; 2000-072883/06.

PS Claim 12; Fig 60; 278bp; English.

XX The present sequence is a human PRO polypeptide (secreted and  
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
CC anti-PRO antibodies are useful for preparation of a medicament useful in  
CC the treatment of a condition which is responsive to the PRO protein,  
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping

XX Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 4; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 28 MASIGQLFWSTISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILSCTFEP 87
DB 1 MASIGQLFWSTISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILSCTFEP 60
QY 88 DIKLSDIVIQLWKEGVGLVHEFEKGEKDELSEODEMFRGRTPAFADQIVGNASIRLKNV 147
DB 61 DIKLSDIVIQLWKEGVGLVHEFEKGEKDELSEODEMFRGRTPAFADQIVGNASIRLKNV 120
QY 148 QLTDAITYKCYIITTSKGNANLEYKTGAFSMPEVAVDYNASSETLRCEAPRMFPQPTVV 207
DB 121 QLTDAITYKCYIITTSKGNANLEYKTGAFSMPEVAVDYNASSETLRCEAPRMFPQPTVV 180
QY 208 WASQVDQGANFSEVSNTSFEINSENVTKVSVLVNTTNTYSCMIENDIAKATGDIKY 267
DB 181 WASQVDQGANFSEVSNTSFEINSENVTKVSVLVNTTNTYSCMIENDIAKATGDIKY 240
QY 268 TSESIKRRSHLQLNSKASLCVSSFFAISMALLPLSPYIMLK 309
DB 241 TSESIKRRSHLQLNSKASLCVSSFFAISMALLPLSPYIMLK 282
```

RESULT 9

AAB99204  
ID AAB99204 standard; protein; 282 AA.

XX AAB99204;

XX 04-SEP-2001 (first entry)

XX Human ovarian tumour-derived antigen O8E #1.

XX Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;

XX antigen; O8E.

XX Homo sapiens.

XX WO200140269-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-US032520.

XX 30-NOV-1999; 99US-00451651.

XX 22-FEB-2000; 2000US-00510662.

XX 10-MAR-2000; 2000US-00523586.

XX 07-APR-2000; 2000US-00545068.

XX 15-MAY-2000; 2000US-00571025.

XX (CORI-) CORIXA CORP.

XX Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;

XX WPI; 2001-356154/37.

XX N-PSDB; AAH55681.

XX Breast tumor polypeptides and the nucleic acids that encode them, useful

PT for the prevention, diagnosis and treatment of breast cancer.

XX Example 3; Page 190; 221bp; English.

XX The present invention relates to human breast tumour protein coding  
CC sequences (see AAH5479-AAH5513, AAH5517-AAH5567 and AAH55682-  
CC AAH55762). The breast tumour protein DNA sequences may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the breast tumour protein e.g. breast cancer.  
CC The present sequence is a human ovarian tumour-derived antigen, which was  
CC used in an example from the present invention

XX Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 4; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 28 MASIGQLFWSTISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILSCTFEP 87
DB 1 MASIGQLFWSTISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILSCTFEP 60
QY 88 DIKLSDIVIQLWKEGVGLVHEFEKGEKDELSEODEMFRGRTPAFADQIVGNASIRLKNV 147
DB 61 DIKLSDIVIQLWKEGVGLVHEFEKGEKDELSEODEMFRGRTPAFADQIVGNASIRLKNV 120
QY 148 QLTDAITYKCYIITTSKGNANLEYKTGAFSMPEVAVDYNASSETLRCEAPRMFPQPTVV 207
DB 121 QLTDAITYKCYIITTSKGNANLEYKTGAFSMPEVAVDYNASSETLRCEAPRMFPQPTVV 180
QY 208 WASQVDQGANFSEVSNTSFEINSENVTKVSVLVNTTNTYSCMIENDIAKATGDIKY 267
DB 181 WASQVDQGANFSEVSNTSFEINSENVTKVSVLVNTTNTYSCMIENDIAKATGDIKY 240
QY 268 TSESIKRRSHLQLNSKASLCVSSFFAISMALLPLSPYIMLK 309
DB 241 TSESIKRRSHLQLNSKASLCVSSFFAISMALLPLSPYIMLK 282
```

RESULT 10

AAB65242  
ID AAB65242 standard; protein; 282 AA.

XX AAB65242;

XX 02-APR-2001 (first entry)

XX Human PRO1291 (UNQ659) protein sequence SEQ ID NO:291.

XX Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;

XX cancer; Chromosomal mapping; gene mapping; tissue typing;

XX diagnostic assay.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US008439.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 07-JUL-1999; 99US-0143048P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 17-AUG-1999; 99US-0149396P.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 08-OCT-1999; 99US-0158663P.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028301.

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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gertltsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AJ, Kijavits IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR MPI: 2001-032160/04.
DR N-PSDB; AAF44205.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 208; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 282 AA;

```

Query Match 90.9%; Score 1431; DB 4; Length 282;  
Best Local Similarity 100.0%; Pred.No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 28 MASIGQILFWISIIIIILAGALALILIGFISGRHSITVTVAASAGNIGEDGILSCTFEP 87
DB 1 MASIGQILFWISIIIIILAGALALILIGFISGRHSITVTVAASAGNIGEDGILSCTFEP 60
QY 88 DIKLSDIVIQLKEGVGLVHEFEKGEKDELSEQDEMERGRVAFADQVIVGNASRLKNV 147
DB 61 DIKLSDIVIQLKEGVGLVHEFEKGEKDELSEQDEMERGRVAFADQVIVGNASRLKNV 120
QY 148 QLTDAAGTYKCYIITTSKGNANLEYKTAGAFSMEPVNTDYNASSETLRCEAPRMFPQPTVV 207
DB 121 QLTDAAGTYKCYIITTSKGNANLEYKTAGAFSMEPVNTDYNASSETLRCEAPRMFPQPTVV 180
QY 208 WASQVDQGANFSEVNTSEFELNENVTMKVSVLYNTTINTNTYSCNIENDIAKATGDIKV 267
DB 181 WASQVDQGANFSEVNTSEFELNENVTMKVSVLYNTTINTNTYSCNIENDIAKATGDIKV 240
QY 268 TESIIRKSHLQILNSKASLGVSSFAISWALLPLSPYLMK 309
DB 241 TESIIRKSHLQILNSKASLGVSSFAISWALLPLSPYLMK 282

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AAE20311
ID AAE20311 standard; protein; 282 AA.
XX
AC AAE20311;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human B7-H8 protein #1.
XX
KW Human; B7-like protein; inflammation; tissue damage; immune disorder;
KW Addison's disease; autoimmune haemolytic anaemia; autoimmune thyroiditis;
KW diabetes mellitus; Crohn's disease; multiple sclerosis; allergy; cancer;
KW rheumatoid arthritis; cardiovascular disorder; nervous system disorder;
KW myocardial ischaemia; ulcerative colitis; reproductive system disorder;
KW Alzheimer's disease; Parkinson's disease; endocrine disorder; hepatitis;
KW diabetes mellitus; Grave's disease; Paget's disease; liver disorder;
KW gastrointestinal disorder; irritable bowel syndrome; cerebral anoxia;
KW dysphagia; hepatomegaly; neurological disease; infectious disease;
KW epilepsy; gene therapy; B7-H8 protein; chromosome 1.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24 /label=Signal_peptide
FT Protein 25..282 /note="Mature B7-H8 protein"
XX
PN WO200202587-A1.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US020917.
XX
PR 30-JUN-2000; 2000US-021513P.
PR 14-AUG-2000; 2000US-0225266P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fiscella M, Ni J, Ruben SM;
XX
DR MPI: 2002-257198/30.
DR N-PSDB; AAD32519.
XX
PT Isolated nucleic acids encoding human B7-like polypeptides, useful for
PT diagnosis and treatment of e.g. inflammation, cancer, immune disorders
PT such as Addison's disease, and cardiovascular disorders such as
PT myocardial ischemias.
XX
PS Example 1; Fig 1; 493pp; English.
XX
CC The present invention relates to novel human B7-like polypeptides and
CC polynucleotides encoding such proteins. Sequences of the invention are
CC used for preventing, treating or ameliorating a medical condition in a
CC mammalian subject. The polynucleotides and polypeptides are administered
CC to subjects having a disorder related to B7-like polypeptides, such as
CC inappropriate or excessive inflammation which can lead to tissue damage
CC or even death, where the inflammation is brought about by the activation
CC of certain cells in the body e.g. T cells and may involve disorders
CC related to immune system. The nucleic acids, proteins, antibodies,
CC agonists and antagonists of the invention are useful in the diagnosis,
CC treatment and prevention of cancer (e.g. cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, urogenital or
CC lung), immune disorders (e.g., Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis, ulcerative colitis),
CC cardiovascular disorders (e.g., myocardial ischaemia), nervous system
CC disorders (Alzheimer's disease, Parkinson's disease), endocrine system
CC disorders (e.g., diabetes mellitus, Graves disease), reproductive system disorders
CC (e.g., cryptorchidism, Paget's disease), gastrointestinal disorders (e.g.,
CC dysphagia, irritable bowel syndrome), liver disorders (e.g., hepatitis,
CC hepatomegaly), neurological diseases (e.g., cerebral anoxia and epilepsy)
CC and infectious diseases such as viral, bacterial, fungal and parasitic

```





KW breast cancer; colorectal cancer; lung cancer; ovarian cancer;  
 KW central nervous system cancer; liver cancer; bladder cancer;  
 KW pancreatic cancer; cervical cancer; melanoma; leukaemia; TAT136.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT /label= Signal\_peptide  
 FT Protein 29..282  
 FT /label= Mature\_TAT136  
 FT /note= "tumour associated antigenic target polypeptide"  
 FT Region 52..58  
 FT /label= N-myristoylation\_site  
 FT Region 112..116  
 FT /label= N-glycosylation\_site  
 FT Domain 119..123  
 FT /label= Immunoglobulin\_domain  
 FT Region 126..132  
 FT /label= N-myristoylation\_site  
 FT Region 160..164  
 FT /label= N-glycosylation\_site  
 FT Region 188..194  
 FT /label= N-myristoylation\_site  
 FT Region 190..194  
 FT /label= N-glycosylation\_site  
 FT Region 196..200  
 FT /label= N-glycosylation\_site  
 FT Region 205..209  
 FT /label= N-glycosylation\_site  
 FT Region 216..220  
 FT /label= N-glycosylation\_site  
 FT Region 220..224  
 FT /label= N-glycosylation\_site  
 FT Domain 258..282  
 FT /label= Transmembrane\_domain  
 MO200216581-A2.  
 PD 28-FEB-2002.  
 PF 14-AUG-2001; 2001WO-US025464.  
 XX  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 22-JUN-2001; 2001US-0088257.  
 PR 22-JUN-2001; 2001WO-US020118.  
 XX  
 PN (GENTH ) GENENTECH INC.  
 PI Gao W, Polakis P, Shou J, Smith V, Soriano R, Williams PM,  
 PI Mu TD, Zhang Z;  
 XX WPI; 2002-280928/32.  
 DR N-PSDB; ABK11744.  
 XX  
 PT Novel isolated antibody which binds to tumor-associated antigenic target  
 PT polypeptide useful for killing cancer cells expressing the polypeptide  
 PT and for treating tumor comprising cells that expresses the polypeptide.  
 XX  
 PS Claim 2, Fig 8, 123pp; English.  
 XX  
 CC The invention describes an isolated antibody which binds to a tumour-  
 CC associated antigenic target (TAT) polypeptide. The antibody is useful  
 CC for killing a cancer cell (such as a breast, colorectal, lung, ovarian,  
 CC central nervous system, liver, bladder, pancreatic, cervical, melanoma or  
 CC leukaemia cell) that expresses a polypeptide with at least 80% identity  
 CC to the TAT polypeptide sequence; treating a tumour comprising cells that  
 CC express a polypeptide with at least 80% identity to the TAT polypeptide  
 CC sequence; determining the presence of a polypeptide having at least 80 %  
 CC identity to the TAT polypeptide sequence in a sample suspected of  
 CC containing the polypeptide; diagnosing the presence of a tumour in a  
 CC mammal, and for antibody dependent enzyme mediated prodruq therapy

CC (ADPRT). This is the amino acid sequence of the tumour associated  
 CC antigenic target polypeptide (TAT) 136, described in the invention  
 XX  
 SQ Sequence 282 AA;  
 Query Match 90.9%; Score 1431; DB 5; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 28 MASLGILFMSIIIIIIAGAILIIFGIGSRHSITVTVAAGNIGEDGILSTFEP 87  
 DB 1 MASLGILFMSIIIIIIAGAILIIFGIGSRHSITVTVAAGNIGEDGILSTFEP 60  
 QY 88 DIKLSDIVIOMLKEGVLAGVHEFEKGEKDELSEDEMFEGRTAVFADQVTVGNASLRKNV 147  
 DB 61 DIKLSDIVIOMLKEGVLAGVHEFEKGEKDELSEDEMFEGRTAVFADQVTVGNASLRKNV 120  
 QY 148 QLTDACTYKCYITITSKKGANLEYKTGAFSMEFVNVDYNASSETLRCEAPRWPPTTV 207  
 DB 121 QLTDACTYKCYITITSKKGANLEYKTGAFSMEFVNVDYNASSETLRCEAPRWPPTTV 180  
 QY 208 WASQVDQGANFSEVSNSTSEFELNSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267  
 DB 181 WASQVDQGANFSEVSNSTSEFELNSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKV 240  
 QY 268 TSEIKRRSHLQLNLSKASLCVSSFFAISWALLPLSPYLMK 309  
 DB 241 TSEIKRRSHLQLNLSKASLCVSSFFAISWALLPLSPYLMK 282  
 RESULT 14  
 ABG95880 standard; protein; 282 AA.  
 XX  
 AC ABG95880;  
 XX  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Human secreted/transmembrane protein PRO1291.  
 XX  
 KW Human; secreted protein; transmembrane protein; anti-rheumatic;  
 KW antiarthritic; osteopathic; sports-related joint problem;  
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002119130-A1.  
 PD 29-AUG-2002.  
 PF 06-DEC-2001; 2001US-00006867.  
 XX  
 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 22-APR-1998; 98US-0082797P.  
 PR 29-APR-1998; 98US-0083495P.  
 PR 15-MAY-1998; 98US-0085579P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088740P.  
 PR 10-JUN-1998; 98US-0088811P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088825P.  
 PR 11-JUN-1998; 98US-0088863P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 19-JUN-1998; 98US-0089952P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 24-JUN-1998; 98US-0090444P.

PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 17-AUG-1998; 98US-0096517P.  
PR 18-AUG-1998; 98US-0096549P.  
PR 18-AUG-1998; 98US-0096559P.  
PR 26-AUG-1998; 98US-009754P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099792P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98US-0099815P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 08-MAR-1999; 99WO-US0105028.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021194.  
PR 22-DEC-1999; 99WO-US030720.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032378.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski EJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX  
DR WPI; 2002-731348/79.  
DR N-PSDB; ABS74407.  
XX  
XX  
PT New isolated secreted and transmembrane PRO polypeptide useful for  
PT modulating biological activity of a cell, or for treating sports-related  
PT joint problems, osteoarthritis or rheumatoid arthritis.  
XX  
PS Claim 20; Fig 60; 399pp; English.  
XX  
CC The invention relates to an isolated secreted and transmembrane PRO  
CC polypeptide having 80 % sequence identity to a sequence appearing as

CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an  
CC extracellular domain of the proteins with their associated signal peptide  
CC or lacking its associated signal peptide. Also included are the nucleic  
CC acids encoding the proteins, vectors, host cells, fusion proteins and  
CC antibodies which specifically bind to the proteins. The proteins are  
CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
CC suspected of containing an A, B, C or D polypeptide, by contacting the  
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
CC and determining the formation of a A/E, B/F, C/G, C/H or D/I polypeptide  
CC conjugate in the sample, where the formation of the conjugate is  
CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
CC H or I polypeptide is labeled with a detectable label or is attached to a  
CC solid support. The proteins are useful for linking a bioactive molecule  
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
CC H or I. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
CC or I, or antibodies against them are useful for modulating a biological  
CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
CC identifying agonists or antagonists, for the preparation of a medicament  
CC useful in the treatment of a condition which is responsive to the  
CC proteins, as molecular weight markers for protein electrophoresis  
CC purposes, and as therapeutic agents for treating sports-related joint  
CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis. Nucleic acids encoding the proteins are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
CC generate transgenic or knockout animals which are useful in the  
CC development and screening of therapeutic useful reagents, for chromosome  
CC identification, and in gene therapy. The antibody is useful as a  
CC therapeutic agent, in a diagnostic assay and for affinity purification of  
CC the protein from recombinant cell culture natural sources. The present  
CC sequence represents a novel secreted or transmembrane protein of the  
CC invention  
XX  
SQ Sequence 282 AA;  
Query Match 90.9%; Score 1431; DB 5; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 MASLQGLFMSIIITIIILAGAILIIGFISGRHSITVTTVASAGNIGEDGILSCTEEP 87  
Db 1 MASLQGLFMSIIITIIILAGAILIIGFISGRHSITVTTVASAGNIGEDGILSCTEEP 60  
QY 88 DIKLSIVIVQMLKEGVLGLVHEFEKGDSEQDEMFGRTAIPADQVIYGNASRLKNV 147  
Db 61 DIKLSIVIVQMLKEGVLGLVHEFEKGDSEQDEMFGRTAIPADQVIYGNASRLKNV 120  
QY 148 QLTDACTYKCYIITSKGGANILEYKTGAFSMEPEVNVYNASSETLRCEAPRFPQPTVV 207  
Db 121 QLTDACTYKCYIITSKGGANILEYKTGAFSMEPEVNVYNASSETLRCEAPRFPQPTVV 180  
QY 208 WASQVDQGANFSEVNTSFEINSENVTKVSVLYNTVINTNTSCMIENDIAKATGDIKV 267  
Db 181 WASQVDQGANFSEVNTSFEINSENVTKVSVLYNTVINTNTSCMIENDIAKATGDIKV 240  
QY 268 TESIIRRSRSHQILNSKASLCVSSFFAISMALPLSPYIMLK 309  
Db 241 TESIIRRSRSHQILNSKASLCVSSFFAISMALPLSPYIMLK 282  
RESULT 15  
AAU76536  
ID AAU76536 standard; protein; 282 AA.  
XX  
AC AAU76536;  
XX

DT 05-JUN-2002 (first entry)  
XX Tumour-associated antigenic target protein, TAT136.  
DE TAT136; Tumour-associated Antigenic Target; tumour; breast cancer;  
XX colorectal cancer; lung cancer; ovarian cancer;  
KW central nervous system cancer; liver cancer; bladder cancer; melanoma;  
XX pancreatic cancer; leukaemia; gene therapy.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..28  
FT Protein /note="Signal sequence"  
FT Protein 29..282  
FT Domain /note="Mature TAT134"  
FT Domain 49..132  
FT Modified-site /note="Immunoglobulin domain"  
FT Modified-site 52..58  
FT Modified-site /note="N-myristoylation site"  
FT Modified-site 112..116  
FT Modified-site /note="Asn is N-glycosylated"  
FT Modified-site 126..132  
FT Modified-site /note="N-myristoylation site"  
FT Modified-site 160..164  
FT Modified-site /note="Asn is N-glycosylated"  
FT Modified-site 190..194  
FT Modified-site /note="Asn is N-glycosylated"  
FT Modified-site 196..200  
FT Modified-site /note="Asn is N-glycosylated"  
FT Modified-site 205..209  
FT Modified-site /note="Asn is N-glycosylated"  
FT Modified-site 216..220  
FT Modified-site /note="Asn is N-glycosylated"  
FT Modified-site 220..224  
FT Modified-site /note="Asn is N-glycosylated"  
FT Domain 258..281  
FT Domain /note="Transmembrane domain"  
XX  
XX WO200216429-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 22-JUN-2001; 2001WO-US020118.  
XX  
XX 24-AUG-2000; 2000WO-US023328.  
XX 26-SEP-2000; 2000US-0235451P.  
XX 01-DEC-2000; 2000WO-US032678.  
XX 28-FEB-2001; 2001WO-US006520.  
XX 01-MAR-2001; 2001WO-US006666.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V;  
XX Wood WI, Wu TD, Zhang Z;  
XX  
XX WPI; 2002-280917/32.  
XX N-PSDB; ABK11091.  
XX  
XX Novel isolated tumor-associated antigenic target polypeptides which are  
XX useful as targets for cancer therapy and diagnosis in mammals.  
XX  
XX  
XX Claim 12; Fig 8; 121pp; English.  
XX  
XX The invention relates to an isolated tumour-associated antigenic target  
XX polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the  
XX polynucleotides (II) encoding them. (II) is useful for diagnosing the  
XX presence of a tumour in a mammal, where the level of expression of (II)  
XX is indicative on the presence of tumour in the mammal from which the test  
XX sample was obtained. Antibody to (I) is useful for killing a cancer cell  
XX (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,  
XX an ovarian cancer cell, a central nervous system (CNS) cancer cell, a  
XX liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a

CC melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides  
CC hybridizing to (II) are useful as diagnostic probes; antisense  
CC oligonucleotide probes or for encoding fragments of full length TAT  
CC polypeptide. (II) is also useful in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA probes, for constructing  
CC hybridisation probes for mapping the gene encoding TAT and for genetic  
CC analysis of individuals with genetic disorders. (II) is also useful for  
CC generating either transgenic animals or knockout animals, and in gene  
CC therapy. The TAT polypeptides and nucleic acids may also be used for  
CC tissue typing and the TAT polypeptides are useful for screening compounds  
CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT  
CC polypeptide (antagonist). The antibody is useful for staging TAT  
CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT  
CC polypeptide from cells, for detection and quantitation of TAT polypeptide  
CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or  
CC Western blot. The antibodies are also useful for treating a TAT-  
CC expressing cancer or alleviating one or more symptoms of cancer in a  
CC mammal. The present sequence represents the amino acid sequence of TAT136  
XX  
SQ Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 5; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2.2e-117;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLQILFMSIISIIIIIIAGALMIIGFISGRHSITVTVAAGNIGEDGILSCTFEP 87  
DB 1 MASLQILFMSIISIIIIIIAGALMIIGFISGRHSITVTVAAGNIGEDGILSCTFEP 60  
QY 88 DIKLSDIVIOWLKEGVLAGVHEFEKQDELSEODEMFEGRITAVFADQYIVGNASLRKNV 147  
DB 61 DIKLSDIVIOWLKEGVLAGVHEFEKQDELSEODEMFEGRITAVFADQYIVGNASLRKNV 120  
QY 148 QLTDAQTYKCYIITSKGNANLEFKTGAFSMPEVNVNDNASSETLRCEAPRMPPOPTVV 207  
DB 121 QLTDAQTYKCYIITSKGNANLEFKTGAFSMPEVNVNDNASSETLRCEAPRMPPOPTVV 180  
QY 208 WASQVDOGANFSEVNTSEPLNSENVTKVSVLYNVINNTSCMIENDIAKATGDIKV 267  
DB 181 WASQVDOGANFSEVNTSEPLNSENVTKVSVLYNVINNTSCMIENDIAKATGDIKV 240  
QY 268 TSEIIRSRSHQLNSKASLCVSSFFAISWALLPLSPYLMK 309  
DB 241 TSEIIRSRSHQLNSKASLCVSSFFAISWALLPLSPYLMK 282

Search completed: May 11, 2004, 16:21:29  
Job time : 61 secs

;; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
;; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
;; FILE REFERENCE: 15966-562 (CURA-62)  
;; CURRENT APPLICATION NUMBER: US/09/651,200  
;; PRIOR APPLICATION NUMBER: 60/152383  
;; PRIOR FILING DATE: 1999-09-03  
;; PRIOR APPLICATION NUMBER: 60/172909  
;; PRIOR FILING DATE: 1999-12-21  
;; PRIOR APPLICATION NUMBER: 60/183578  
;; PRIOR FILING DATE: 2000-02-18  
;; NUMBER OF SEQ ID NOS: 25  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 4  
;; LENGTH: 441  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-651-200-4

Query Match 15.6%; Score 246; DB 4; Length 441;  
Best Local Similarity 26.2%; Pred. No. 1.2e-16;  
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

QY 19 QIRWESPAMASLGOI-----LF--WSIIIIIIILAGAILITGFI---SGRHS 63  
Db 82 EVFWODGQGVPLTGNVTTSQMANEQGLFDVHSLRVILGANGTYSCLVRNPVLQDASHS 141  
QY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIKLSDIYIOMLKEGVILGLV 107  
Db 142 VTTTPQRSPTGAVEVQVPEDPVVALVGTDTATLHCSFSPEPGFSLTQNLIMWLTDTQQLV 201  
QY 108 HEFKGKDELSEQDEMFRGTAVPADQYIVGNASLRKLVQLTDAITYKCYITTSKSGN 167  
Db 202 HSFTGGRD-----QGSAYANRTALFPDLAQGNASLRQVRVADEGSFTCF--VSIRDFGS 256  
QY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEAPRWFPOPTVWASQVDOGANFSEV 221  
Db 257 AAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITTCSSYRGYPBAEVFW--QDGGVPLTGN 314  
QY 222 SNTSFELNSENVTKVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT 268  
Db 315 VTTT-OMANEQGLFDVHSLRVILGANGTYSCLVRNPVLQDASHSVTIT 363

RESULT 6  
US-09-651-200-6  
; Sequence 6, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651,200  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/183578  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 534  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-651-200-6

Query Match 15.6%; Score 246; DB 4; Length 534;  
Best Local Similarity 26.2%; Pred. No. 1.6e-16;

Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;  
QY 19 QIRWESPAMASLGOI-----LF--WSIIIIIIILAGAILITGFI---SGRHS 63  
Db 175 EVFWODGQGVPLTGNVTTSQMANEQGLFDVHSLRVILGANGTYSCLVRNPVLQDASHS 234  
QY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIKLSDIYIOMLKEGVILGLV 107  
Db 235 VTTTPQRSPTGAVEVQVPEDPVVALVGTDTATLHCSFSPEPGFSLTQNLIMWLTDTQQLV 294  
QY 108 HEFKGKDELSEQDEMFRGTAVPADQYIVGNASLRKLVQLTDAITYKCYITTSKSGN 167  
Db 295 HSFTGGRD-----QGSAYANRTALFPDLAQGNASLRQVRVADEGSFTCF--VSIRDFGS 349  
QY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEAPRWFPOPTVWASQVDOGANFSEV 221  
Db 350 AAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITTCSSYRGYPBAEVFW--QDGGVPLTGN 407  
QY 222 SNTSFELNSENVTKVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT 268  
Db 408 VTTT-OMANEQGLFDVHSLRVILGANGTYSCLVRNPVLQDASHSVTIT 456

RESULT 7  
US-09-651-200-24  
; Sequence 24, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651,200  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/183578  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 534  
; TYPE: PRT  
; ORGANISM: Unknown  
; OTHER INFORMATION: Description of Unknown Organism: Sequence  
; OTHER INFORMATION: mz5020.protein from Figure 4.  
US-09-651-200-24

Query Match 15.6%; Score 246; DB 4; Length 534;  
Best Local Similarity 26.2%; Pred. No. 1.6e-16;  
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

QY 19 QIRWESPAMASLGOI-----LF--WSIIIIIIILAGAILITGFI---SGRHS 63  
Db 175 EVFWODGQGVPLTGNVTTSQMANEQGLFDVHSLRVILGANGTYSCLVRNPVLQDASHS 234  
QY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIKLSDIYIOMLKEGVILGLV 107  
Db 235 VTTTPQRSPTGAVEVQVPEDPVVALVGTDTATLHCSFSPEPGFSLTQNLIMWLTDTQQLV 294  
QY 108 HEFKGKDELSEQDEMFRGTAVPADQYIVGNASLRKLVQLTDAITYKCYITTSKSGN 167  
Db 295 HSFTGGRD-----QGSAYANRTALFPDLAQGNASLRQVRVADEGSFTCF--VSIRDFGS 349  
QY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEAPRWFPOPTVWASQVDOGANFSEV 221  
Db 350 AAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITTCSSYRGYPBAEVFW--QDGGVPLTGN 407  
QY 222 SNTSFELNSENVTKVSVLYNVT-INNTYSCMIENDIAK--ATGDIKVT 268

Db 408 VTTT-QMANEGGLFDVHSLRVVLGANGTYSCLVRNPVLQDDAHGSVTTIT 456

## RESULT 8

US-09-651-200-2  
; Sequence 2, Application US/09651200  
; Patent No. 6429303  
; GENERAL INFORMATION:  
; APPLICANT: Green et al  
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 15966-562 (CURA-62)  
; CURRENT APPLICATION NUMBER: US/09/651,200  
; CURRENT FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/152383  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/172909  
; PRIOR FILING DATE: 1999-12-21  
; PRIOR APPLICATION NUMBER: 60/183578  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-651-200-2

Query Match 15.6%; Score 245; DB 4; Length 340;

Best Local Similarity 27.8%; Pred. No. 9.6e-17;  
Matches 72; Conservative 50; Mismatches 101; Indels 36; Gaps 11;

QY 38 SIISIIIIILAGAILIIGFGI---SGRHSITYTTVAS-----AGNIGEDGI 80  
DB 12 SIIRVLGANGTYSCLVRNPVLQDDAHGSVTTITPQSPGAVEVQVBEDEVVALVGTDAI 71  
QY 81 LSCFP--EPVUKISDIYQWKEGVGLVHEFEKGEKDELSEQDENFRGRTAVPADQIVG 138  
DB 72 LHGFSPEPFGSLQNLINWOLDTKQLVHSTEGRD-----QGSAYANRITALLFPDLAQS 127  
QY 139 NASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGA-FSMPEVNVVDYN-----ASSET 192  
DB 128 NASIRLQVRVAABEGSFTCF-VSIRDFGSAASLVQAAPYSKPSMTLEPNKDLRPGDTVT 186  
QY 193 LRCEAPRFPQPTVVMASQVDQGANFSEVSNFSFELNSENVTMKVSVLYNVT-INNTYS 251  
DB 187 ITGSSYRGYFEAEVFW-QDQGQVPLTGNVTTT-QMANEGGLFDVHSLRVVLGANGTYS 243  
QY 252 CMIEINDIAK--ATGDIKVT 268  
DB 244 CLVRNPVLQDDAHGSVTTIT 262

## RESULT 9

US-09-910-174B-28  
; Sequence 28, Application US/09910174B  
; Patent No. 6630575  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
; TITLE OF INVENTION: Family and Uses Thereof  
; FILE REFERENCE: 35800/236924  
; CURRENT APPLICATION NUMBER: US/09/910,174B  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 09/620,461  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28

; LENGTH: 315  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-910-174B-28

Query Match 15.2%; Score 238.5; DB 4; Length 315;  
Best Local Similarity 26.9%; Pred. No. 4e-16;  
Matches 65; Conservative 46; Mismatches 112; Indels 19; Gaps 7;

QY 37 WSIIIIIIILAGAILIIGFGISGRHSITYTTVASAGNIGEDGILSCFP--EPDIKLSDI 94  
DB 5 WGPSPVGVCTATAG-VLCCLTGAVEVQVSEDPVALVDTDAITLRCSPBEPFSLAQL 63  
QY 95 VIQWLKEGVGLVHEFEKGEKDELSEQDENFRGRTAVPADQIVGNASIRLKNVQLTDAGT 154  
DB 64 NLIMQLDTKQLVHSTEGRD-----QGSAYSNRITALLFPDLVQGNASIRLQVRVTTDEGS 119  
QY 155 YKCYIITSKGNANLEYKTGAFSMPEVNVVDYN-----ASSETLRCEAPRFPQPTVYVA 209  
DB 120 YTCFVSIQDFPSAAVSLQVAPYSKPSMTLEPNKDLRPGNMVTTITCSSYQYFEAEVFW- 178  
QY 210 SQVDQGANFSEVSNFSFELNSENVTMKVSVLYNVT-INNTYSCMIEINDIAK--ATGDIK 266  
DB 179 ---KDQGGVPLTGNVTSQMANERGLFDVHSLRVVLGANGTYSCLVRNPVLQDDAHGSVT 235  
QY 267 VT 268  
DB 236 IT 237

RESULT 10  
US-09-620-461-28  
; Sequence 28, Application US/09620461  
; Patent No. 6635750  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
; TITLE OF INVENTION: Family and Uses Thereof  
; FILE REFERENCE: 5800-149  
; CURRENT APPLICATION NUMBER: US/09/620,461  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 315  
; TYPE: PRT  
; ORGANISM: Mus  
US-09-620-461-28

Query Match 15.2%; Score 238.5; DB 4; Length 315;  
Best Local Similarity 26.9%; Pred. No. 4e-16;  
Matches 65; Conservative 46; Mismatches 112; Indels 19; Gaps 7;

QY 37 WSIIIIIIILAGAILIIGFGISGRHSITYTTVASAGNIGEDGILSCFP--EPDIKLSDI 94  
DB 5 WGPSPVGVCTATAG-VLCCLTGAVEVQVSEDPVALVDTDAITLRCSPBEPFSLAQL 63  
QY 95 VIQWLKEGVGLVHEFEKGEKDELSEQDENFRGRTAVPADQIVGNASIRLKNVQLTDAGT 154  
DB 64 NLIMQLDTKQLVHSTEGRD-----QGSAYSNRITALLFPDLVQGNASIRLQVRVTTDEGS 119  
QY 155 YKCYIITSKGNANLEYKTGAFSMPEVNVVDYN-----ASSETLRCEAPRFPQPTVYVA 209  
DB 120 YTCFVSIQDFPSAAVSLQVAPYSKPSMTLEPNKDLRPGNMVTTITCSSYQYFEAEVFW- 178  
QY 210 SQVDQGANFSEVSNFSFELNSENVTMKVSVLYNVT-INNTYSCMIEINDIAK--ATGDIK 266  
DB 179 ---KDQGGVPLTGNVTSQMANERGLFDVHSLRVVLGANGTYSCLVRNPVLQDDAHGSVT 235  
QY 267 VT 268



Db 236 IT 237

## RESULT 11

US-09-910-174B-18  
; Sequence 18, Application US/09910174B  
; Patent No. 6630375; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575e1 Members of the B7  
; FILE REFERENCE: 35800/236924  
; CURRENT APPLICATION NUMBER: US/09/910,174B  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 09/620,461  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-910-174B-18

## Query Match

14.2%; Score 223; DB 4; Length 513;  
Best Local Similarity 26.4%; Pred. No. 3.4e-14;  
Matches 69; Conservative 44; Mismatches 108; Indels 40; Gaps 10;

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QY 62 HSITVTVASAGNI-----GEGGILSCTEFPEDIKSDIVIQWLKEGVGLVHEFKGDEL 117
Db 27 HSAQSFVLGSPGPIIAMVGEDADLPCHLFTPTMSAETMELKWSSSLRQVNVYADGKEVE 86
QY 118 SEQDENFRGRFAVFADQVITGNASLRKLVQLTAGTYKCYITTSKGNANLEYKTGAF 177
Db 87 DRQAPYRGRTSILRDGITAGKALRIHNVYASDSGKYLCPDGDGFYEKALVELKYAAL 146
QY 178 SMPENVVD---YNASSETLRCEAPRMFPQPTVWVASQVDQGANFSEVSNTPSLNSENVT 234
Db 147 G-SDLHVDVKYKDGSIHLECRSTGWYPOQIQMSN--NKGEN--IPTVEAPVAVAGVG 200
QY 235 MKVV--SVLYNVTINNVTSCMIENDIAKATGDIKVTSEIKRSHLQLNSKASLCVSS- 291
Db 201 LYAVASVIMRSGSGEGVSGCTI-----RSSLLGLEKTAISISIA DP 240
QY 292 FF--AISM--ALLPLSPYML 308
Db 241 FFRSAQRWIALARTLPVLL 261
```

## RESULT 12

US-09-620-461-18  
; Sequence 18, Application US/09620461  
; Patent No. 6635750; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750e1 Members of the B7  
; FILE REFERENCE: 5800-149  
; CURRENT APPLICATION NUMBER: US/09/620,461  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-620-461-18

## Query Match

14.2%; Score 223; DB 4; Length 513;

Best Local Similarity 26.4%; Pred. No. 3.4e-14;  
Matches 69; Conservative 44; Mismatches 108; Indels 40; Gaps 10;

```
QY 62 HSITVTVASAGNI-----GEGGILSCTEFPEDIKSDIVIQWLKEGVGLVHEFKGDEL 117
Db 27 HSAQSFVLGSPGPIIAMVGEDADLPCHLFTPTMSAETMELKWSSSLRQVNVYADGKEVE 86
QY 118 SEQDENFRGRFAVFADQVITGNASLRKLVQLTAGTYKCYITTSKGNANLEYKTGAF 177
Db 87 DRQAPYRGRTSILRDGITAGKALRIHNVYASDSGKYLCPDGDGFYEKALVELKYAAL 146
QY 178 SMPENVVD---YNASSETLRCEAPRMFPQPTVWVASQVDQGANFSEVSNTPSLNSENVT 234
Db 147 G-SDLHVDVKYKDGSIHLECRSTGWYPOQIQMSN--NKGEN--IPTVEAPVAVAGVG 200
QY 235 MKVV--SVLYNVTINNVTSCMIENDIAKATGDIKVTSEIKRSHLQLNSKASLCVSS- 291
Db 201 LYAVASVIMRSGSGEGVSGCTI-----RSSLLGLEKTAISISIA DP 240
QY 292 FF--AISM--ALLPLSPYML 308
Db 241 FFRSAQRWIALARTLPVLL 261
```

## RESULT 13

US-08-724-394A-4  
; Sequence 4, Application US/08724394A  
; Patent No. 5872237; GENERAL INFORMATION:  
; APPLICANT: Feder, John N.  
; APPLICANT: Kronmal, Gregory S.  
; APPLICANT: Laufer, Peter M.  
; APPLICANT: Ruddy, David A.  
; APPLICANT: Thomas, Winston  
; APPLICANT: Teuchinshai, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
; TITLE OF INVENTION: Sequences and Antibodies Thereof  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,394A  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 017957-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..540  
; OTHER INFORMATION: /note= "BTF5"



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 11, 2004, 16:17:11 ; Search time 21 Seconds  
(without alignments)  
1415.390 Million cell updates/sec

Title: US-09-827-271-392  
Perfect score: 1574  
Sequence: 1 HASAHASGRQRQLHSASTQI.....SSFAISWALLPLSPYLMK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 28366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219.5	13.9	526	2	A37821 butyrophilin - bov
2	211.5	13.4	526	2	S70587 butyrophilin precu
3	171.5	10.9	487	2	S65133 butyrophilin - mou
4	168.5	10.7	391	2	T09058 butyrophilin homol
5	163.5	10.4	299	2	I46590 CD80 precursor - r
6	153	9.7	275	2	JC7604 CD86 spliced varia
7	151	9.6	339	2	T28138 Ig V-region-like B
8	150.5	9.6	340	2	A55717 Ig V-region-like B
9	150	9.5	247	2	T28137 myelin/oligodendro
10	147.5	9.4	329	1	A48754 B7-2 antigen - hum
11	147.5	9.4	330	2	I46691 CD86 precursor - r
12	147	9.3	218	2	B47712 myelin/oligodendro
13	146.5	9.3	372	2	C39371 Ig V-region-like B
14	146	9.3	398	2	A39371 Ig V-region-like B
15	144	9.1	247	2	S58394 myelin/oligodendro
16	143.5	9.1	309	2	I49522 gene B7-2 protein
17	140.5	8.9	246	2	A47712 myelin/oligodendro
18	135	8.6	761	1	IUHUNG neural cell adhesi
19	134.5	8.5	503	2	JC5287 SHP substrate-1 pr
20	133	8.4	1091	1	IUCHNL neural cell adhesi
21	132.5	8.4	853	1	IUBONC neural cell adhesi
22	130.5	8.3	725	1	IUMSNG neural cell adhesi
23	130.5	8.3	1033	2	S19247 cell adhesion prot
24	130.5	8.3	1115	1	IUSMNL neural cell adhesi
25	128.5	8.2	858	1	IURUNC neural cell adhesi
26	127	8.1	946	1	A47299 ror-related recept
27	126.5	8.0	765	1	C42632 cell adhesion mole
28	126.5	8.0	812	2	B42632 cell adhesion mole
29	126.5	8.0	932	2	A42632 cell adhesion mole

30	126.5	8.0	1088	1	IUXNL	neural cell adhesi
31	125.5	8.0	1018	2	JC4211	neural adhesion pr
32	124	7.9	309	2	I49503	B-lymphocyte activ
33	123.5	7.8	725	2	JE0099	neural cell adhesi
34	123.5	7.8	5175	2	T20992	hypothetical prote
35	123.5	7.8	5198	2	T43290	hemictinal precurs
36	122.5	7.8	871	1	I48696	protein-tyrosine k
37	122.5	7.8	881	1	I48697	protein-tyrosine k
38	121.5	7.7	1612	2	T30805	ducl1 protein - mo
39	121	7.7	321	2	I54766	B-lymphocyte activ
40	121	7.7	365	2	JC7780	coxackie- and ade
41	121	7.7	1091	2	S01998	contractin precuso
42	120	7.6	215	2	A57843	sodium channel bet
43	120	7.6	288	2	A45803	B-cell-restricted
44	120	7.6	333	2	A31923	amalgam protein pr
45	118	7.5	321	2	D39371	Ig V-region-like B

## ALIGNMENTS

### RESULT 1

butyrophilin - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 05-Nov-1999  
C:Accession: A37821  
R:Jack, L.J.W.; Mather, I.H.  
J. Biol. Chem. 265, 14481-14486, 1990  
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein  
A:Reference number: A37821; MID:90354441; PMID:2387867  
A:Accession: A37821  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-526 <UAC>  
A:Cross-references: GB:M3551; NID:g1763685; PIDN:AAB39766.1; PID:g162773  
C:Keywords: transmembrane protein

Query Match 13.9%; Score 219.5; DB 2; Length 526;  
Best Local Similarity 25.0%; Pred. No. 4.5e-09;  
Matches 49; Conservative 48; Mismatches 94; Indels 5; Gaps 4;

QY	75	IGEDGILSTFEPDIDKSDIVIQWLKEGVJGLVHEFKGDELSEODEMRGRVAFADQ	134
DB	42	VGEDAEELPCRLSPNVSAKGMELRWERKVPVAFVSRGQEGHEMAEYRGVSLVEDH	101
QY	135	VIVGNASRLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF-SMEPVNVVDYNASSE-T	192
DB	102	IAEGSVAVRIGEVKASDDGERCFRQDENVEBAIVHLKVAALGSDPHLSMKVQESGEIQ	161
QY	193	LRCEAPRPFQPTVVWASQVDGANGFSEVSNTPFLNSENVTMKVSVLVNTINNTVSC	252
DB	162	LECTSVGVYFEPQVQW--RTIRGEFPPSMSESRLNDEEGLFTVRAAVITRDSSMKV--SC	218
QY	253	MIENDIAKATGDIKVT	268
DB	219	CIRNLLIGQEKDVEVS	234

### RESULT 2

butyrophilin precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jul-2000  
C:Accession: S70587  
R:Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.  
Biochim. Biophys. Acta 1306, 1-4, 1996  
A:Title: Cloning and sequence analysis of human butyrophilin reveals a potential recep  
A:Reference number: S70587; MID:96201696; PMID:8611614  
A:Accession: S70587  
A>Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-526 <TAY>  
A:Cross-references: EMBL:U9576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083

Query Match 13.4%; Score 211.5; DB 2; Length 526;  
Best Local Similarity 26.6%; Pred. No. 1.8e-08;  
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGEDGILCTFEPPDIKLSDIVIQWLKEGVGLVHEFEKGEKDELSEQDEMFRGRTAVFADQ 134  
DB 42 VGEDAEILPCRLSPNASEHLELTKRCKVSPAVLVHRDGEQEAQMPREYRGRTLVQDG 101  
QY 135 VIVGNASLRKLVQLTDACTYKCYIITSKGNANLEYKTGAF-SMPEVNVVYNASSE-T 192  
DB 102 IAKGRVALRIRGVSDGGEYTCFFREDGSYEELVHLKVVALGSDPHISMQVQENGELIC 161  
QY 193 LRCEAPRWFPOPTVWASQVDQGANFSEVNTSFEINSENVTKVVSVLVNTVINTYSC 252  
DB 162 LECTSVGWYEPQVQW--RTSGEKFPSTSE-SRNPDEGLFTVAASVLIIRDISTKNTVC 218  
QY 253 MIEN 256  
DB 219 YIQN 222

## RESULT 3

S65133  
butyrophilin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999

C:Accession: S65133

R:ishi, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.

Biochim. Biophys. Acta 1245, 285-292, 1995

A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophilin specifically associat

A:Reference number: S65133; MUID:96125722; PMID:8541302

A:Accession: S65133

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-487 <ISH>

A:Cross-references: GB:S80642; NID:g1246078; PIDN:AAB35893.1; PID:g1246079

Query Match 10.9%; Score 171.5; DB 2; Length 487;  
Best Local Similarity 22.4%; Pred. No. 1.9e-05;  
Matches 44; Conservative 51; Mismatches 92; Indels 9; Gaps 4;

QY 77 EDGILCTFEPPDIKLSDIVIQWLKEGVGLVHEFEKGEKDELSEQDEMFRGRTAVFADQYI 136  
DB 8 DDALITCGFSPNASSEYELMLFRQRTSTAVLLYRDQEQGQQTETKRGRTATAGLL 67  
QY 137 VGNASLRKLVQLTDACTYKCYIITSKGNANLEYKTGAF-SMPEVNVVYNASSE-TLR 194  
DB 68 DGRATLIRVDRPSDQGEYRCLFKDNDFEERAAVYIKVAAGSDPQISMTVQENGEMELR 127  
QY 195 CEAPRWFPOPTVWASQVDQGANFSEVNTSFEINSENVTKVVSVLVNTVINTYSC 252  
DB 128 CTSSGWYEPQVQWRT-----GNREMLPSTSDSKKNEEGHFTVAVSMMLSDSSIKNMSC 182  
QY 253 MIENDIAKATGDIKVT 268  
DB 183 CIQNIILGQGEVEIS 198

## RESULT 4

T09058

butyrophilin homolog - mouse (fragment)

N:Alternate names: butyrophilin-like protein

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999

C:Accession: T09058

R:Rowen, L.; Mahitras, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc

submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: Z16543

A:Accession: T09058

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-391 <ROW>

A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564946

A:Note: BAC 29N7

C:Genetics:

A:Map position: 17

A:Note: butyrophilin-like

A:Note: Intron positions not resolved (incomplete sequence)

Query Match 10.7%; Score 168.5; DB 2; Length 391;  
Best Local Similarity 26.3%; Pred. No. 2.4e-05;  
Matches 52; Conservative 45; Mismatches 82; Indels 19; Gaps 8;

QY 76 GEDGILCTFEPPDIKLSDIVIQWLKEGVGLVHEFEKGEKDELSEQDEMFRGRTAVFADQ 134  
DB 26 GREALIPCSVLPVNVNEMELKRNFRSAVLVYRDQEQKREQMTETYSWRTSLVXDQ 85  
QY 135 VIVGNASLRKLVQLTDACTYKCYIITSKGNANLEYKTGAF-SMPEVNV-DYNASSET 192  
DB 86 FHQGTAAVRIONIQASDSGLYICFRMGQFHEBALLELKVAAAGSVPEVHIKGPEDGGVC 145  
QY 193 LRCEAPRWFPOPTVWASQVDQGANFSEVNTSFEINSENV-----TMKV--SVLYN 243  
DB 146 VVCMTSGWYEPQVHWRD--SRGEKFT----ASLEIHGEDAQGLFRTETSLVVRDSSVRN 199  
QY 244 VTINNTYSCMTENDIAKA 261  
DB 200 V-ICSTFNSILQGEKAWA 216

## RESULT 5

I46690

CD80 precursor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 29-Sep-1999

C:Accession: I46690

R:isomo, T.; Seto, A.

Immunogenetics 42, 217-220, 1995

A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecul

A:Reference number: I46689; MUID:95369849; PMID:7642234

A:Accession: I46690

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-259 <ISO>

A:Cross-references: GB:D49843; NID:g755096; PIDN:BA08643.1; PID:g755097

C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 10.4%; Score 163.5; DB 2; Length 299;  
Best Local Similarity 25.3%; Pred. No. 4.1e-05;  
Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

QY 40 ISIIITAGALALITFGISGRHSITVTVAASAGNIGEDGILCTFEPPDI-KLSDIVIQW 98  
DB 19 LCLILALAG---LHPSGIS-----QVTK-----SVKEMALSGDYNISIDELARMRIYW 65  
QY 99 LKEG--VLGLVHEFEKGEKDELSEQDEMFRGRTAVFADQYIVGNASLRKLVQLTDACTYK 156  
DB 66 QKDQQWVLSIT-----SGQVEYWP--YKRT--FPD--IINNTSLMILALRLSDKGYTT 114  
QY 157 CYIITSKGNANLEYKTGA-----FSMPEV-----NVYNASSETLRCEAPRWFPOPT 205  
DB 115 C-VVQKNENGSRFRRHLSVTLSIRADFVPVPSITDIGHDPNV--KRIRCSASGSPFPER 171  
QY 206 VVWASQVDQGANFSEVNTSFEINSENVTKVVSVLVNTVINTYSCMTENDIAKATBD 264  
DB 172 LAW---MEDGELNAV-NTVQDDIDTELYSVSSELDFTVNTNHSIVCLIK-----YGE 221  
QY 265 IKYTE---SEIKRSHLQILNSKASLGVSSFPALSWALLPLSPYLML 308  
DB 222 LSVQIRPWSKPKQEPIDQLP-----FWVLIIPVSGALVL 256

RESULT 6  
UC7604  
CD86 spliced variant CD86 deltaTM isoform - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 18-Nov-2002  
C:Accession: J07604  
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.  
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001  
A>Title: Identification of an alternatively spliced variant of human CD86 mRNA.  
A:Reference number: J07604; MUID:21092744; PMID:11162656  
A:Accession: J07604  
A:Molecule type: mRNA  
A:Residues: 1-275 <MAG>  
C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory  
C:Genetics:  
A:Gene: cd86deltaTM  
C:Superfamily: B-lymphocyte restricted antigen B7  
C:Keywords: Immune response

	Query Match	9.7%; Score 153; DB 2;	Length 275;
	Best Local Similarity	23.7%; Pred. No. 0.00024;	
	Matches      Conservative	44; Mismatches 99; Indels 82; Gaps 14.	
QY	50 IALIGFGISGRHSITVTTVTASAGNIGEDGLSCFE--EPDIKLSDIVIQMLKEGVLGV	107	
Db	6 ILFWAFLILSGAAPLKIQAY-----FNETADLPCCPANSQNQSISELVWFWDQENTL-VL	59	
QY	108 HEFYEGKDELSEODEMFRGRGTAVFPADVIVGNASIRLNKVOLTDACTKYCIITSKGKG-	166	
Db	: :  :: :		
	60 NEVYLGEKEPFDSVHSKYMGRTPSDS----SWTLRLHLNIQIKDXYGLYCIIHHKKPTGM	114	
QY	167 ----NANLEKYTG-FSMEPV---NVDNASSSETLRCEAPRMWFOPTVVMAAQVDQGAM	217	
Db	:		
	115 IRIHQMNSSELVANFSSQPRIPIINITEENVYI-NLTCSLHGYPEE----	160	
QY	218 FSEVSNTSFELNSENAVTKV-----VSVLVNVTI-----NNYSAMIEN	256	
Db	:		
	161 -----KKMSVLRTKNSTIERDEIMQKSQDVNTELYDVISLSVPDPVTSNMTHICILET	216	
QY	257 DIAK-----ATGDIKYTESE-IKRSHQL-----INSKSLCVSS	291	
Db	:		
	217 DKETLLSPPSGISGINTMEREESQOTGREKIHIPEPRSDAEORVFASKSKTSCDKS	271	

RESULT 7  
T28138  
Ig V-region-like B-G antigen, isoform 2 - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
C:Accession: T28138  
R:Milne, S.; Kaufman, J.; Beck, S.  
submitted to the EMBL Data Library, May 1998  
A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp  
A:Reference number: Z20475  
A:Accession: T28138  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-339 <MIL>  
A:Cross-references: EMBL:AL023516; PIDN:CA18959.1  
A:Experimental source: clone CB12  
C:Genetics:  
A:Gene: B-G 2  
A:Map position: 16  
A:Introns: 34/1, 148/1, 183/1, 189/1, 196/1, 203/1, 210/1, 217/1, 224/1, 231/1, 239/1, 2

```

Query Match      9.6%; Score 151; DB 2; Length 339;
Best Local Similarity 21.7%; Pred. No. 0.00044;
Matches 56; Conservative 46; Mismatches 90; Indels 66; Gaps 10.

QY      63 SIYTTVASAGNIGEDGILSCFEE--DKLSDIYIQMLKEGVTLVHFEKGEKDELSEQ 120
Db      42 SLRTATAI-----VGQDVVLRICQLSECKDAWSSD--IRMTQHRTSFVHHYONGED--LEQ 92

```

[illegible]

RESULT 8  
 T28137  
 Ig V-region-like B-G antigen, isoform 1 - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C/Accession: T28137  
 R./Milne, S.; Kaufman, J.; Beck, S.  
 Submitted to the EMBL Data Library, May 1998  
 A./Description: DNA sequencing and analysis of the chicken major histocompatibility comp  
 A./Reference number: Z20475  
 A./Accession: T28137  
 A./status: preliminary; translated from GB/EMBL/DDBJ  
 A./molecule type: DNA  
 A./Residues: 1-340 <MIL>  
 A./Cross-references: EMBL:AL023516; PIDN:CA18958.1  
 A./Experimental source: clone cB12  
 C./Genetics:  
 A./Gene: B-G 2  
 A./Map position: 16  
 A./Intons: 34/1; 148/1; 183/1; 190/1; 197/1; 204/1; 211/1; 218/1; 225/1; 232/1; 240/1;

```
Query Match      9.6%; Score 150.5; DB 2, Length 340;  
Best Local Similarity 32.4%; Pred.No. 0.00048;  
Matches    35; Conservative   22; Mismatches   40; Indels   11; Gaps    4
```

OY    63 SITVTVASAGNIGEDGILSTFEF--DILSLDIVIQMLKEGVGLVHEFKKDELSEQ    120  
     |:|:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db    42 SLRFTAI-----VGQDVVLRCQLSPCKDAWSSD--IRMIQRTSGEVHHYONGED--LEQ    92  
  
OY    121 DEMERGRTAVPADQIVGNASLRLENVQLDAGTKCYITLSKGKNNA    168  
     :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db    93 MEEXXGRLLRLRKGSIDGMIDLRIITAVTSDSGSCAYCAGDGADADA    140

```

RESULT 9
A55717
myelin/oligodendrocyte glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
C:Accession: A55717; #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
R:Daubas, P.; Pham-Dinh, D.; Dautigny, A.
Genomics 23, 36-41, 1994
A:Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein gene
A:Reference number: A55717; MUID:95130110; PMID:7829100
A:Accession: A55717
A:Molecule type: DNA
A:Residues: 1-247 <DAV>
A:Cross-references: GB:L29498
R:Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.; Pontarotti, P.; Roeckel, N
Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
A:Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobulin
A:Reference number: A47712; MUID:93376728; PMID:8367453
A:Accession: C47712
A:Molecule type: mRNA
A:Residues: 30-95, 'E', 97-247 <PHA>
A:Cross-references: GB:L20942; NID:G399568; PIDN:AAA03180.1; PID:G399569

```





C:Genetics:  
A:Gene: MOG  
C:Function:  
A:Description: may be involved in lipid interaction; may be involved in cell-cell commun  
C:Keywords: glycoprotein; myelin; transmembrane protein  
F:1-216/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>  
F:122-150/Domain: transmembrane #status predicted <TM1>  
F:175-200/Domain: transmembrane #status predicted <TM2>  
F:31/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	9.3%	Score 147;	DB 2;	Length 218;
Best Local Similarity	28.3%	Pred. No. 0.0005;		
Matches	28;	Conservative	47;	Indels 0;
				Gaps 0;

QY IIGEDILSCFFEPDIKLSIDIVIQWKEGVLGVHEEEGGKKLSEDEMEFGRTAVADQ 134  
75 :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::  
Db 16 VGDDELPCISPGKNATVGEVGVIYRSPFSRKRVHLFRNGKODAEQAPFYRRTELKES 75

```

QY      135 VIVGNASRLKNVQLTDAGTYKCYIIITSGKGNANLEYK 173
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      76 IGEKVALRIQNVRFSDEGGYTCFRDHSYQEAAVELK 114

```

## RESULT 13

Ig V-region-like B-G antigen 11/4 precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 23-Mar-1993  
 C:Accession: C39371  
 R:Miller, M.M.; Goto, R.; Young, S.; Chitrivella, J.; Hawke, D.; Miyada, C.G.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991  
 A:Title: Immunoglobulin variable-region-like domains of diverse sequence within the major  
 A:Reference number: A39371; MUID:91239571; PMID:1903541  
 A:Accession: C39371  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-372 <MIL>  
 A:Cross-references: GB:M61861

Query Match 9.3%; Score 146.5; DB 2; Length 372;

Best Local Similarity 20.7%; Pred No. 0.0011;  
Matches 59; Conservative 51; Mismatches 88; Indels 87; Gaps 9;

QY 63 SIFATTVASAGNIGEDGILSTFEERPIKLSIVICWKEGVGLVHEFEKEGDELSQDE 122  
 42 SLRTATL-----VGQDVLRCHLCPECKDAMRLDIRMILLQSSGFVHHYONGVD-LGQWE 95  
 Db

[illegible]

QY 174 -----TGAF-----SMEVANDYNNSSSETLRCEA 197  
 |||  
 Db 155 HPWKALAVVTTILVGSFVAINFLCKKAQSRRLKRDAPALAEIDISGISAENLK--- 211

```

0Y      198 PRWFQPTVWASQVDGANSSEVASTSFELNSENTMKV-----VSVLV 242
          : : : : : : : : : : : : : : : : : : : : : : : :
Db      212 -----OLASKUNENAEVEDCNSLKDCCSEMGVADIKELAAKLEEYIAVNR 262

```

Qy 243 NVTINNTYSCMIENDIAKAGDIKYTESEIKR---RSHIQLNSK 284  
 ||:|| :||:::|:|  
 Db 263 NTKLNN-----IAAKLAQQFTYLEKQHSQFHRHFPQMDLSAVNOK 302

## RESULT 14

Ig V-region-like B-G antigen 14/8 precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C.Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 01-Dec-2000  
 C.Accession: A39371, B39371  
 R.Miller, M.M.; Goto, R.; Young, S.; Chirivella, J.; Hawke, D.; Miyada, C.G.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 4377-4381, 1991  
 A>Title: Immunoglobulin variable-region-like domains of diverse sequence within the maj

A:Reference number: A39371; MUID:91239571; PMID:1903541  
A:Accession: A39371  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-398 <MIT>  
A:Cross-references: GB:M61860; NID:G211241; PIDN:AAA48619.1; PID:G211243  
A:Accession: B39371  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-385,387-398 <MI2>  
A:Cross-references: GB:M61864; NID:G211264; PIDN:AAA48650.1; PID:G211266

Query Match	9.3%	Score 146	DB 2	Length 398
Best Local Similarity	33.1%	Pred. No. 0.0013		
Matches 40	Conservative 25	Mismatches 42	Indels 14	Gaps 7

```
Qy      63 SIATVTVASAGNIGEDGILCTFEF--DIKSIDVIQWLKEGLGLVHEFRKDELTSEQ 120
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      42 SLRTVTA-----VGQDVLRCHLSPCCKDVNSD--IRWIQRRSLVHYHYNGVD--LGM 93
```

QY 122 DEMRGRTAVFADQYIVGNASLRLKNVQLDAGTKYCIITSKGKNA--NLEKYKGAFS 178  
 Db 94 EE-YKGRTELLRDGSDGNDLRLTAATVTSDDSGSYSCAVDGDAAVAEAVNMLEV-SDPFS 151

QY	179	M	179
Db	152	M	152

## RESULT 15

myelin/oligodendrocyte glycoprotein precursor - human  
 C1species: Homo sapiens (man)  
 C1date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 08-Oct-1999  
 C1accession: S58394.; S78430.; S78431.; I56513  
 R1Hilton, A.A.; Slavin, A.J.; Hilton, D.J.; Bernard, C.C.A.  
 J. Neurochem. 65, 309-318, 1995  
 A1title: Characterization of cDNA and genomic clones encoding human myelin oligodendrocyte glycoprotein precursor  
 A1reference number: S58394.; MUID:95310943.; PMID:7790876

A;Accession: S58394  
A;Molecule type: mRNA

A;Cross-references: EMBL:X74511; NID:G984146; PIDN:CA052617.1; PID:g984144  
A;Experimental source: adult medulla  
A;Accession: S78430

A:Residues: 1-197, 'GKFRHV' <HI>  
A:Note: truncated protein is probably not functionally active  
A:Accession: S78431

A:Residues: 1-247 <HD>  
A:Cross-references: GB:X74511, NID:g984146; PIDN:CAA52617.1, PID:g984147  
R:Diam-Dinh, D.; Alliquant, B.; Ruberg, M.; Della Gaspera, B.; Nussbaum, J.L.; Dautigny

A:Title: Characterization and expression of the cDNA coding for the human myelin/oligoc  
A:Reference number: 156513, MUIR:95054056, PMID:7964757  
A:Accession: 156513

A:Molecule type: mRNA  
A:Residues: 1-247 <RS>  
A:cross-references: GB:S73472; NID:ig688175; PID:ig688176

A; Gene: MOG  
C; Function:  
A; Descripti

A;description: may be involved in lipid interaction; may be involved in cell-cell communication  
C;keywords: alternative splicing; glycoprotein; myelin / transmembrane protein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>  
F;351-119/Domain: transmembrane #status predicted <TM1>  
F;304-229/Domain: transmembrane #status predicted <TM2>  
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 144; DB 2; Length 247;

Best Local Similarity 20.8%; Pred. No. 0.001;  
Matches 49; Conservative 39; Mismatches 80; Indels 68; Gaps 6;  
QY 28 MASLSQILFWISITIIIL-----AGATALLIGFISGRHSITVTVASAGNIGED 78  
Db 1 MASLSRPSLPSCLCSTLLLLLOVSSSYAGQPRV-----IGPRHPIRAL-----VGDE 48  
QY 79 GILSCTFEPDIXLSDIVIQWLKEGVLGIVHEFEKGEDELSEQDEMRGRTAVPADQVIIG 138  
Db 49 VELPCRIISPGKNAITGMEVGWYRPPFSRVVHLRYNGKDQDGDQAPERYGRTELLKDAIGEG 108  
QY 139 NASIRLKNVQLTDAGTYKCYIITSKKGKGNANLEYKTGAFSPMEPVAVDYNASSETLRCEAP 198  
Db 109 KVTLRIRNVRFSDGEGFTCFEFDHSYQBEAAME-----LKVEDP 147  
QY 199 RMFPQPTVVMASQVDQGANFSEVSNTSFEINSENVTMKVVSU-LYNTVINNTYSQM 253  
Db 148 FYWVSPGVL-----VLLAVLPVLLQITVGLVFICL 178

Search completed: May 11, 2004, 16:23:29  
Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 16:16:20 ; Search time 46 Seconds  
(without alignments)  
219.459 Million cell updates/sec

Title: US-09-827-271-392  
Perfect score: 1574  
Sequence: 1 HASAHASGRQRQHSASTQI.....SSFAISWALLPLSPYIMLK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SPREMBL\_25:\*
- 2: sp\_archaea:\*
- 3: sp\_bacteria:\*
- 4: sp\_fungi:\*
- 5: sp\_human:\*
- 6: sp\_invertebrate:\*
- 7: sp\_mammal:\*
- 8: sp\_mbc:\*
- 9: sp\_organelle:\*
- 10: sp\_plant:\*
- 11: sp\_prodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	90.9	282	4	Q7Z7D3
2	1425	90.5	282	4	Q9H6B2
3	1261.5	80.1	283	11	Q7TPH5
4	1257.5	79.9	283	11	Q7TSP5
5	1253.5	79.6	283	11	Q8K091
6	512	32.5	285	13	Q7ZY30
7	448	28.5	275	13	Q8AVV1
8	247	15.7	316	4	Q9BXV1
9	246	15.6	388	4	Q8NC34
10	246	15.6	533	4	Q8NCB6
11	246	15.6	534	4	Q8NB18
12	235	14.9	316	11	Q8VE98
13	232	14.7	316	11	Q7TPB4
14	225	14.3	220	4	Q9NM06
15	225	14.3	414	4	Q9UM44
16	223	14.2	495	4	Q9HCY1

17	223	14.2	513	4	Q00481	Q00481 homo sapien
18	222.5	14.1	347	4	Q9H730	Q9H730 homo sapien
19	220	14.0	280	13	Q73716	Q73716 grus americ
20	219.5	13.9	286	6	Q46535	Q46535 bos taurus
21	215.5	13.7	304	6	Q9BE26	Q9BE26 macaca fasc
22	215.5	13.7	731	4	P78409	P78409 homo sapien
23	213.5	13.6	584	4	Q00478	Q00478 homo sapien
24	209.5	13.3	526	4	Q9H458	Q9H458 homo sapien
25	208.5	13.2	334	4	Q9NR44	Q9NR44 homo sapien
26	207.5	13.2	319	4	Q00477	Q00477 homo sapien
27	207.5	13.2	334	4	Q9BU81	Q9BU81 homo sapien
28	207.5	13.2	357	4	Q15338	Q15338 homo sapien
29	207.5	13.2	359	4	P78410	P78410 homo sapien
30	204	13.0	350	4	Q99420	Q99420 homo sapien
31	199.5	12.7	290	11	Q9EP73	Q9EP73 mus musculu
32	196.5	12.5	492	11	Q8C008	Q8C008 mus musculu
33	196	12.5	296	13	Q42404	Q42404 gallus gall
34	195.5	12.4	275	11	Q9JK39	Q9JK39 mus musculu
35	193	12.3	334	4	Q96AV7	Q96AV7 homo sapien
36	193	12.3	527	4	Q00475	Q00475 homo sapien
37	192	12.2	329	6	Q9XSX6	Q9XSX6 felis silve
38	192	12.2	332	6	Q9GMZ7	Q9GMZ7 felis silve
39	192	12.2	332	6	Q95L16	Q95L16 felis silve
40	191.5	12.2	289	11	Q8K3J3	Q8K3J3 meriones un
41	188.5	12.0	290	4	Q9NZQ7	Q9NZQ7 homo sapien
42	188	11.9	567	4	Q96KV6	Q96KV6 homo sapien
43	186	11.8	529	4	P78408	P78408 homo sapien
44	183	11.6	336	4	Q8WVY5	Q8WVY5 homo sapien
45	183	11.6	523	4	Q00480	Q00480 homo sapien

ALIGNMENTS

ID	Q7Z7D3	PRELIMINARY:	PRT:	282 AA.
AC	Q7Z7D3;			
DT	01-OCT-2003 (TREMBlrel. 25, Created)			
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Immune costimulatory protein B7-H4.			
DI	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sica G.L., Choi I.-H., Zhu G., Tamada K., Wang S.-D., Tamura H.,			
RA	Chapoval A.I., Flies D.B., Bajorath J., Chen L.,			
RT	"Immune inhibition by human B7-H4."			
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY280972; AAP37283.1; -; 1C9C565A9242E78C CRC64;			
SQ	SEQUENCE 282 AA; 30878 MW; 1C9C565A9242E78C CRC64;			

Query Match	Best Local Similarity	Score	90.9%;	DB 4;	Length 282;
Matches	282;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	28	MASLGQILFMSIISIIIIAGAILIIFGIGSGHSTIVTVASAGNIGEDGILSCTEEP	87		
DB	1	MASLGQILFMSIISIIIIAGAILIIFGIGSGHSTIVTVASAGNIGEDGILSCTEEP	60		
QY	88	DIKLSDIVIQWLKEGVLGLVHEFEKGDSEBQDEMFRGRTAVFADQYIVGNASLRANV	147		
DB	61	DIKLSDIVIQWLKEGVLGLVHEFEKGDSEBQDEMFRGRTAVFADQYIVGNASLRANV	120		
QY	148	QUTDAGTYKCIYITISKSGKANLEKGTGAFSPMEVNVVDNASSETLRCEAPRMPQPTV	207		
DB	121	QUTDAGTYKCIYITISKSGKANLEKGTGAFSPMEVNVVDNASSETLRCEAPRMPQPTV	180		
QY	208	WASQVQGANSEVNTSFEINSEVNTKVVSVLYNTTINNTYSCEIENDIAKATGDIKY	267		

Db 181 WASQVDGANGSEVSNTESELENSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKY 240  
QY 268 TSESIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYLMK 309  
Db 241 TSESIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYLMK 282

## RESULT 2

Q9HEB2 PRELIMINARY; PRT; 282 AA.  
AC Q9HEB2; 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hypothetical protein F4J22418.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Oktani R., Ota T., Suzuki Y., Ohashi M., Nishi T., Shibahara T.,  
RA Tanaka T., Nakamura Y., Isegai T., Sugano S.;  
RT "NEO human cDNA sequencing project."  
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
EMBL; AK026071; BAB15349.1; -  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR007110; Ig-like.  
DR SMART; SM00409; Ig.1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 282 AA; 30893 MW; 6F906699A1E9DB4 CRC64;

Query Match 90.5%; Score 1425; DB 4; Length 282;  
Best Local Similarity 99.6%; Pred. No. 3.1e-108;  
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILCTFEP 87  
Db 1 MASLGQILFWSIISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILCTFEP 60  
QY 88 DIKLSDIVIOWLKEGVLGLVHEFEKGEDELSEODEMFRGRTAVFADQVTVGNASIRLKNV 147  
Db 61 DIKLSDIVIOWLKEGVLGLVHEFEKGEDELSEODEMFRGRTAVFADQVTVGNASIRLKNV 120  
QY 148 QLTADAGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYASSSETLRCEAPRWFPPQPTV 207  
Db 121 QLTADAGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYASSSETLRCEAPRWFPPQPTV 180  
QY 208 WASQVDGANGSEVSNTESELENSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKY 267  
Db 181 WASQVDGANGSEVSNTESELENSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKY 240  
QY 268 TSESIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYLMK 309  
Db 241 TSESIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYLMK 282

## RESULT 3

Q7TPH5 PRELIMINARY; PRT; 283 AA.  
AC Q7TPH5; 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE B7S1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=22703430; PubMed=12818166;  
RA Prasad D.V., Richards S., Mai X.M., Dong C.;  
RT "B7S1, a novel B7 family member that negatively regulates T cell  
activation."  
RL Immunity 18:863-873 (2003).  
DR EMBL; AY322147; AAP88965.1; -  
SQ SEQUENCE 283 AA; 30847 MW; A97F17461857850B CRC64;

Query Match 80.1%; Score 1261.5; DB 11; Length 283;  
Best Local Similarity 88.0%; Pred. No. 6.9e-95;  
Matches 249; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 28 MASLGQILFWSIISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILCTFEP 87  
Db 1 MASLGQILFWSIISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILCTFEP 60  
QY 88 DIKLSDIVIOWLKEGVLGLVHEFEKGEDELSEODEMFRGRTAVFADQVTVGNASIRLKNV 147  
Db 61 DIKLSDIVIOWLKEGVLGLVHEFEKGEDELSEODEMFRGRTAVFADQVTVGNASIRLKNV 120  
QY 148 QLTADAGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYASSSETLRCEAPRWFPPQPTV 207  
Db 121 QLTADAGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYASSSETLRCEAPRWFPPQPTV 180  
QY 208 WASQVDGANGSEVSNTESELENSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKY 267  
Db 181 WASQVDGANGSEVSNTESELENSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKY 240  
QY 268 TSESIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYLMK 309  
Db 241 TSESIKRRSHLQILNSKASLCVSSFFAISMALLPLSPYLMK 283

## RESULT 4

Q7TSP5 PRELIMINARY; PRT; 283 AA.  
AC Q7TSP5; 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Immune costimulatory protein B7-H4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=BALB/c;  
RA Sica G.L., Choi I.-H., Zhu G., Tamada K., Wang S.-D., Tamura H.,  
RA Chapoval A.I., Flies D.B., Bajorath J., Chen L.;  
RT "Immune inhibition by mouse B7-H4."  
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY280973; AAP37284.1; -  
SQ SEQUENCE 283 AA; 30875 MW; 7E2F174618578519 CRC64;

Query Match 79.9%; Score 1257.5; DB 11; Length 283;  
Best Local Similarity 87.6%; Pred. No. 1.5e-94;  
Matches 248; Conservative 13; Mismatches 21; Indels 1; Gaps 1;

QY 28 MASLGQILFWSIISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILCTFEP 87  
Db 1 MASLGQILFWSIISIIIIILAGALALIGFGISGRHSITVTVASAGNIGEDGILCTFEP 60  
QY 88 DIKLSDIVIOWLKEGVLGLVHEFEKGEDELSEODEMFRGRTAVFADQVTVGNASIRLKNV 147  
Db 61 DIKLSDIVIOWLKEGVLGLVHEFEKGEDELSEODEMFRGRTAVFADQVTVGNASIRLKNV 120  
QY 148 QLTADAGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYASSSETLRCEAPRWFPPQPTV 207  
Db 121 QLTADAGTYKCYIITSKGGKGNANLEYKTGAFSMPEVNVVDYASSSETLRCEAPRWFPPQPTV 180  
QY 208 WASQVDGANGSEVSNTESELENSENVTKVSVLYNVTINNTYSCMIENDIAKATGDIKY 267



```
QY 87 PDIKLSDIVIQMLKEGVLGVHFEKGEDELSEODEMFRGRTAVADQIVGNASLRKN 146
DB 61 PDITQAN-NIQWEKVGISGVVYKYEKSKSLNQGONADFKGRTSLFSEIKSGNASLKLQ 119
QY 147 VQLTDACTKCYITTSKKGANLEVTGAFSPMEVNVVNASSETLRCEAPRFPQPTV 206
DB 120 IELSDAGTYKCIITNSKGTGEBDTLTFKVGAYTDVVVT---SPSNDTLRCTSSDMYPKPNV 176
QY 207 VNASQVDGAGANSEVSNTSFEINSENVTKVSVLVNTTNTYSCMIENDIAKATGDIK 266
DB 177 TWENSED--NINTITKTYTPALFNLT-DVTSELHGAQDVEYTCXIRHVLAAQAVGVM 233
QY 267 VTSEIKRRSHQLNLSKASLCV 289
DB 234 LTRDGLQTTARLEVNSVDPLSV 256

RESULT 8
Q9BXRL PRELIMINARY; PRT; 316 AA.
AC Q9BXRL;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Costimulatory molecule.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2116383; PubMed=11224528;
RA Chapoval A.I., Ni J., Lau J.S., Wilcox R.A., Flies D.B., Liu D.,
RA Dong H., Sica G.L., Zhu G., Tamada K., Chen L.;
RT "B7-H3: A costimulatory molecule for T cell activation and IFN-gamma
RT production."
RL Nac. Immun. 2:269-274(2001).
EMBL; AF302102; AK15438.1; -.
DR GO: GO:0008263; P:cell proliferation; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR SEQUENCE 316 AA; 33791 MW; FF97007F191CCF61 CRC64;

Query Match 15.7%; Score 247; DB 4; Length 316;
Best Local Similarity 28.5%; Pred. No. 5.8e-12;
Matches 74; Conservative 46; Mismatches 106; Indels 34; Gaps 10;
```

```
RESULT 9
Q9NC34 PRELIMINARY; PRT; 388 AA.
ID Q9NC34
AC Q9NC34;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90516.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Makamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NEDO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK074997; BAC11344.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00408; IGc2; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 388 AA; 41768 MW; 44A59B9E3AB3DCD3 CRC64;

Query Match 15.6%; Score 246; DB 4; Length 388;
Best Local Similarity 26.2%; Pred. No. 9.4e-12;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;
```



[1]  
RN SEQUENCE FROM N.A.  
RP Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,  
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Nishimura K.,  
RT "NEDO human cDNA sequencing project";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074849; BAC11243.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGc1; 2.  
DR SMART; SM00408; IGc2; 4.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR Hypothetical protein; Immunoglobulin domain.  
KW SEQUENCE 533 AA; 57179 MW; FC7E3E3A84F56A56 CRC64;

Query Match 15.6%; Score 246; DB 4; Length 533;  
Best Local Similarity 26.2%; Pred. No. 1.5e-11;  
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;  
QY 19 QIRWEPSPAMASLGQI-----LF--WSIIISIIILAGATALLIGFGI---SGRHS 63  
DB 175 EVFWQDQGQGVPLTGNVTTSGMANEQGLFDVHSILRVLGANGTYSCLVNNPVLQDDAHSS 234  
QY 64 ITVTTVAS-----AGNIGEDGILCTF--EPDIKLSDIVIQLKRGVLTGIV 107  
DB 235 VTTTPQRSPTGAVEVQPEPDPVALVGTDLTRCSFSPSPGSLAQNLNLTQTLTKQLV 294  
QY 108 HEPKEGDELSEODEMERGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGN 167  
DB 295 HSTEGRD---QGSAYANRTALFPDLLAQGNASLRLQVRVADGSGFTCF-VSIRDFGS 349  
QY 168 ANLEYKTGA-FSMPEVNVQVY---ASSETLRCEAPRFPQPTVYMASQVDQGANFSEV 221  
DB 350 AAVSLQVAAPYSKPSMTLEPKDLRPGDVTITCSSYRGYPEAEVFW--QDGGQVPLTGN 407  
QY 222 SNTSFEINSEVNTMKVSVLYNVT--INNTYSCMIENDIAK--ATGDIKYT 268  
DB 408 VTTTS-QMANEQGLFDVHSILRVLGANGTYSCLVNNPVLQDDAHGSVTTT 456

RESULT 11  
Q8NB18 PRELIMINARY; PRT; 534 AA.  
AC Q8NB18;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein NT2RP3001861.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,  
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,  
RA Nagahara K., Sugano S., Isogai T.,  
RT "HRI human cDNA sequencing project";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK075549; BAC11692.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003598; Ig\_c2.

DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGc1; 2.  
DR SMART; SM00408; IGc2; 4.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR Hypothetical protein; Immunoglobulin domain.  
KW SEQUENCE 534 AA; 57265 MW; 0FB1A65948417BBA CRC64;

Query Match 15.6%; Score 246; DB 4; Length 534;  
Best Local Similarity 26.2%; Pred. No. 1.5e-11;  
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;  
QY 19 QIRWEPSPAMASLGQI-----LF--WSIIISIIILAGATALLIGFGI---SGRHS 63  
DB 175 EVFWQDQGQGVPLTGNVTTSGMANEQGLFDVHSILRVLGANGTYSCLVNNPVLQDDAHSS 234  
QY 64 ITVTTVAS-----AGNIGEDGILCTF--EPDIKLSDIVIQLKRGVLTGIV 107  
DB 235 VTTTPQRSPTGAVEVQPEPDPVALVGTDLTRCSFSPSPGSLAQNLNLTQTLTKQLV 294  
QY 108 HEPKEGDELSEODEMERGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGN 167  
DB 295 HSTEGRD---QGSAYANRTALFPDLLAQGNASLRLQVRVADGSGFTCF-VSIRDFGS 349  
QY 168 ANLEYKTGA-FSMPEVNVQVY---ASSETLRCEAPRFPQPTVYMASQVDQGANFSEV 221  
DB 350 AAVSLQVAAPYSKPSMTLEPKDLRPGDVTITCSSYRGYPEAEVFW--QDGGQVPLTGN 407  
QY 222 SNTSFEINSEVNTMKVSVLYNVT--INNTYSCMIENDIAK--ATGDIKYT 268  
DB 408 VTTTS-QMANEQGLFDVHSILRVLGANGTYSCLVNNPVLQDDAHGSVTTT 456

RESULT 12  
Q8VE98 PRELIMINARY; PRT; 316 AA.  
AC Q8VE98;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to B7 homolog 3 (B7-H3).  
GN 6030411F23RIK OR A0U16588 OR B7H3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.,  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Suh W.-K., Chung S., Bray M., Yoshinaga S.K.,  
RT "The B7 family member B7-H3 preferentially downregulates Th1-mediated  
immune responses";  
RT Nat. Immunol. 0:0-0(2003).  
DR EMBL; BC019436; AAH19436.1; -  
DR MGI; MGI:2143194; AAP04007.1; -  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
SQ SEQUENCE 316 AA; 34001 MW; 7BA30B1E67F55827 CRC64;

Query Match 14.9%; Score 235; DB 11; Length 316;  
Best Local Similarity 27.7%; Pred. No. 5.6e-11;  
Matches 67; Conservative 46; Mismatches 111; Indels 18; Gaps 8;

```

QY 37 WSIISIIITLAGAIALIIFGIGSRHSITVTVASAGNIGEDGILSCTF--EPDIKLSDI 94
DB 5 WGGPSVGVCTRLAG-VLCLCLGAVEQVSEDPVALVDIDATLRCFSFSPGSLAQL 63
QY 95 VIOWLKEGVLAGVHEFEKEDLSEODEMFRGTAVFADQVIVGNASLRKXVOLTDAGT 154
DB 64 NLIMQULTDTKQLVHSFTFGRD---QGSAYSNRTALFPDLVQGNASLRLOQVRVTDGGS 119
QY 155 YKCYIITSKGNANLEKYTGAFSMPEVNVN---ASSETLRCEAPRFPQPTVWMA 209
DB 120 YTCFVSIOQFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVITITCSSYQGYPEAEVFWK 179
QY 210 SQVDQGANSEVSNSTSFELNSENVTMKVSVLYNVT-INNTYSCEIENDIAK--ATGDIK 266
DB 180 D--GQGVPLTGNVTS-QMANERGLFDVHSVLRVLGANGTSCVLRNPVLQDAHGSVT 236
QY 267 VT 268
DB 237 IT 238

```

## RESULT 13

```

QY 37 WSIISIIITLAGAIALIIFGIGSRHSITVTVASAGNIGEDGILSCTF--EPDIKLSDI 94
DB 5 WGGPSVGVCTRLAG-VLCLCLGAVEQVSEDPVALVDIDATLRCFSFSPGSLAQL 63
QY 95 VIOWLKEGVLAGVHEFEKEDLSEODEMFRGTAVFADQVIVGNASLRKXVOLTDAGT 154
DB 64 NLIMQULTDTKQLVHSFTFGRD---QGSAYSNRTALFPDLVQGNASLRLOQVRVTDGGS 119
QY 155 YKCYIITSKGNANLEKYTGAFSMPEVNVN---ASSETLRCEAPRFPQPTVWMA 209
DB 120 YTCFVSIOQFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVITITCSSYQGYPEAEVFWK 179
QY 210 SQVDQGANSEVSNSTSFELNSENVTMKVSVLYNVT-INNTYSCEIENDIAK--ATGDIK 266
DB 180 D--GQGVPLTGNVTS-QMANERGLFDVHSVLRVLGANGTSCVLRNPVLQDAHGSVT 236
QY 267 VT 268
DB 237 IT 238

```

Query Match 14.7%; Score 232; DB 11; Length 316;  
Best Local Similarity 27.2%; Pred. No. 9.8e-11;  
Matches 66; Conservative 44; Mismatches 113; Indels 20; Gaps 8;

```

QY 37 WSIISIIITLAGAIALIIFGIGSRHSITVTVASAGNIGEDGILSCTF--EPDIKLSDI 94
DB 5 WGGPSVGVCTRLAG-VLCLCLGAVEQVSEDPVALVDIDATLRCFSFSPGSLAQL 63
QY 95 VIOWLKEGVLAGVHEFEKEDLSEODEMFRGTAVFADQVIVGNASLRKXVOLTDAGT 154
DB 64 NLIMQULTDTKQLVHSFTFGRD---QGSAYSNRTALFPDLVQGNASLRLOQVRVTDGGS 119
QY 155 YKCYIITSKGNANLEKYTGAFSMPEVNVN---ASSETLRCEAPRFPQPTVWMA 209
DB 120 YTCFVSIOQFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVITITCSSYQGYPEAEVFWK 179
QY 210 SQVDQGANSEVSNSTSFELNSENVTMKVSVLYNVT-INNTYSCEIENDIAK--ATGDIK 266
DB 179 ---KDQGLPLTGNVTSQMANERGLFDVHSVLRVLGANGTSCVLRNPVLQDAHGSV 235
QY 266 KVT 268
DB 236 TIT 238

```

## RESULT 14

```

QY 37 WSIISIIITLAGAIALIIFGIGSRHSITVTVASAGNIGEDGILSCTF--EPDIKLSDI 94
DB 5 WGGPSVGVCTRLAG-VLCLCLGAVEQVSEDPVALVDIDATLRCFSFSPGSLAQL 63
QY 95 VIOWLKEGVLAGVHEFEKEDLSEODEMFRGTAVFADQVIVGNASLRKXVOLTDAGT 154
DB 64 NLIMQULTDTKQLVHSFTFGRD---QGSAYSNRTALFPDLVQGNASLRLOQVRVTDGGS 119
QY 155 YKCYIITSKGNANLEKYTGAFSMPEVNVN---ASSETLRCEAPRFPQPTVWMA 209
DB 120 YTCFVSIOQFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVITITCSSYQGYPEAEVFWK 179
QY 210 SQVDQGANSEVSNSTSFELNSENVTMKVSVLYNVT-INNTYSCEIENDIAK--ATGDIK 266
DB 179 ---KDQGLPLTGNVTSQMANERGLFDVHSVLRVLGANGTSCVLRNPVLQDAHGSV 235
QY 266 KVT 268
DB 236 TIT 238

```

```

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein FLJ20685.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ileal mucosa;
RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
RA Shihabara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK006922; BAA91323.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hypothetical protein.
SQ SEQUENCE 220 AA; 24979 MW; 66967620E130B515 CRC64;

```

Query Match 14.3%; Score 225; DB 4; Length 220;  
Best Local Similarity 31.1%; Pred. No. 2.2e-10;  
Matches 61; Conservative 32; Mismatches 81; Indels 22; Gaps 7;

```

QY 73 GNIGEDGILSCTFEPDIKLSDIVIOWLKEGVLAGVHEFEKEDLSEODEMFRGTAVFA 132
DB 41 GRUDEDIILPSSFE--RGEVVIHWKYQDSY-KVHSYKSGSDHESQDPRYANRTSLFY 96
QY 133 DQIVGNASLRKXVOLTDAGTYKCYITISKGNANLEKYTGAFSMPEVNVNASSST 192
DB 97 NEIQNGNASLFRFRVSLDEGIYTCYGTAIQVITNKVVLKVGVELTPVWKYEKRNTEF 156
QY 153 LREAPRFPQPTVWASQVQGA---NFSV-SNTSFELNSENVTMKVSVLYNVT-I 246
DB 157 LICSLSVYPRPIITW--XMDNTPISNNMETGSLDSFESINP-----LNITGS 204
QY 247 NNTYSCEIENDIAKAT 262
DB 205 NSSYECTIENSLKQT 220

```

## RESULT 15

```

QY 37 WSIISIIITLAGAIALIIFGIGSRHSITVTVASAGNIGEDGILSCTF--EPDIKLSDI 94
DB 5 WGGPSVGVCTRLAG-VLCLCLGAVEQVSEDPVALVDIDATLRCFSFSPGSLAQL 63
QY 95 VIOWLKEGVLAGVHEFEKEDLSEODEMFRGTAVFADQVIVGNASLRKXVOLTDAGT 154
DB 64 NLIMQULTDTKQLVHSFTFGRD---QGSAYSNRTALFPDLVQGNASLRLOQVRVTDGGS 119
QY 155 YKCYIITSKGNANLEKYTGAFSMPEVNVN---ASSETLRCEAPRFPQPTVWMA 209
DB 120 YTCFVSIOQFDSAAVSLQVAAPYSKPSMTLEPNKDLRPGNMVITITCSSYQGYPEAEVFWK 179
QY 210 SQVDQGANSEVSNSTSFELNSENVTMKVSVLYNVT-INNTYSCEIENDIAK--ATGDIK 266
DB 179 ---KDQGLPLTGNVTSQMANERGLFDVHSVLRVLGANGTSCVLRNPVLQDAHGSV 235
QY 266 KVT 268
DB 236 TIT 238

```



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 11, 2004, 16:01:45 ; Search time 17 Seconds  
(without alignments)  
946.452 Million cell updates/sec

Title: US-09-827-271-392  
Perfect score: 1574  
Sequence: 1 HASAHASGRQDHSASTQI.....SSFAISWLLPLSPYLMLK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	215.5	13.7	526	1	BUTY_BOVIN
2	211.5	13.4	526	1	BUTY_HUMAN
3	178.5	11.3	524	1	BUTY_MOUSE
4	163.5	10.4	299	1	CD80_RABIT
5	152	9.7	245	1	MOG_RAT
6	150.5	9.6	246	1	MOG_MOUSE
7	147.5	9.4	302	1	ICOL_HUMAN
8	147.5	9.4	329	1	CD86_HUMAN
9	147.5	9.4	330	1	CD86_RABIT
10	144	9.1	247	1	MOG_HUMAN
11	143.5	9.1	309	1	CD86_MOUSE
12	140.5	8.9	246	1	MOG_BOVIN
13	135	8.6	761	1	NCA2_HUMAN
14	135	8.6	848	1	NCA1_HUMAN
15	134.5	8.5	503	1	SHS1_HUMAN
16	132.5	8.4	853	1	NCA1_BOVIN
17	131	8.3	1091	1	NCA1_CHICK
18	130.5	8.3	725	1	NCA2_MOUSE
19	130.5	8.3	1115	1	NCA1_MOUSE
20	128.5	8.2	858	1	NCA1_RAT
21	126.5	8.0	1088	1	NCA1_XENLA
22	125.5	8.0	298	1	JAM2_HUMAN
23	124	7.9	306	1	CD80_MOUSE
24	123	7.8	365	1	CXAR_MOUSE
25	121	7.7	333	1	AMAL_DROME
26	121	7.7	1010	1	CONT_CHICK
27	120	7.6	215	1	CIB2_RAT
28	120	7.6	288	1	CD80_HUMAN
29	120	7.6	365	1	CXAR_HUMAN
30	119	7.6	323	1	DIMI_CAEEL
31	115.5	7.3	509	1	SHS1_RAT
32	115.5	7.3	1092	1	NCA2_XENLA
33	114.5	7.3	322	1	ICOL_MOUSE

34	113.5	7.2	1336	1	VGR1_RAT	P53767	rattus norv
35	113.5	7.2	1461	1	NEO1_HUMAN	O92859	homo sapien
36	113	7.2	359	1	LACH_DROME	O24372	drosophila
37	112.5	7.1	337	1	OPCW_CHICK	O98892	gallus gall
38	112.5	7.1	1018	1	CONT_HUMAN	Q12860	homo sapien
39	112.5	7.1	1020	1	CONT_MOUSE	P12960	mus musculu
40	110	7.0	1036	1	AXO1_CHICK	P28685	gallus gall
41	109.5	7.0	513	1	AXO1_MOUSE	P97797	m protein-t
42	109.5	7.0	1021	1	CONT_RAT	O63198	rattus norv
43	109.5	7.0	1377	1	NEO1_RAT	P97603	rattus norv
44	107.5	6.8	351	1	CD2_HUMAN	P06729	homo sapien
45	106.5	6.8	204	1	CTX2_HUMAN	Q96H03	homo sapien

## ALIGNMENTS

RESULT 1

ID	BUTY_BOVIN	STANDARD	FRT	526 AA.
AC	P18892; O18955; O18959;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).			
GN	BTN1A1 OR BTN.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.			
RX	MEDLINE=90354441; PubMed=2387867;			
RA	Jack U.J.W., Mather I.H.;			
RT	"Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein expressed in mammary tissue and secreted in association with the milk-fat globule membrane during lactation.";			
RL	J. Biol. Chem. 265:14481-14486(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Holstein-Friesian;			
RA	Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,			
RL	Mather I.H., Wilkins R.J.;			
RN	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
RP	[3]			
RC	SEQUENCE FROM N.A.			
RA	TISSUE=Blood;			
RL	Seyfert H.-M., Iuethen F.;			
RN	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RP	[4]			
RC	CARBOHYDRATE-LINKAGE SITES.			
RA	MEDLINE=95293916; PubMed=7775382;			
RT	Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;			
RL	"Site-specific glycosylation of bovine butyrophilin.";			
CC	J. Biochem. 117:147-157(1995).			
CC	-!- FUNCTION: May function in the secretion of milk-fat droplets. It may act as a specific membrane-associated receptor for the association of cytoplasmic droplets with the apical plasma membrane.			
CC	-!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in association with the milk-fat-globule membrane during lactation.			
CC	-!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG family.			
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way			

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M35551; AAB39766.1; -  
DR EMBL; AP005497; AAB62989.1; -  
DR EMBL; Z93323; CAB07533.1; -  
DR PIR; A37821; A37821.  
DR InterPro; IPR001870; B302.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG V.  
DR InterPro; IPR006574; PRY.  
DR InterPro; IPR003877; SPRY\_receptor.  
DR Pfam; PF00047; IG; 1.  
DR Pfam; PF00622; SPRY; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00589; PRY; 1.  
DR SMART; SM00449; SPRY; 1.  
DR PROSITE; PS50835; IG-LIKE; 2.  
DR Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.  
KW SIGNAL  
FT CHAIN 1 26  
FT DOMAIN 27 526 BUTYROPHILIN.  
FT TRANSMEM 27 242 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 243 269 POTENTIAL.  
FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 27 140 IG-LIKE V-TYPE 1.  
FT DOMAIN 148 234 IG-LIKE V-TYPE 2.  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).  
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (HYBRID).  
FT CONFLICT 35 35 Q -> P (IN REF. 3).  
FT CONFLICT 230 230 E -> D (IN REF. 1).  
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;  
  
Query Match 13.7%; Score 215.5; DB 1; Length 526;  
Best Local Similarity 24.5%; Pred. No. 1.3e-09;  
Matches 48; Conservative 49; Mismatches 94; Indels 5; Gaps 4;  
  
QY 75 IGEDGILSTFEEDIKLSDIVIQWLMKEGVLGVHFEKGEKDELSEODEMFRGRTAVFADQ 134  
DB 42 VGEDAELPCRLSPNVAKGMELRMFEKVPSPAVFVSREGQEGEMAEYRGRTSLVEDH 101  
  
QY 135 VIVGNASLRKLVQTDAGTYKCYITTSKGNANLEYKTGAF-SMPEVNVYNASSE-T 192  
DB 102 IAGGSVAVRIQEKASDGEYCFPRDENTEEALVHLKVAALGSDPHISMVQESGEIQ 161  
  
QY 193 LRCEAPRMFPQPTVWVASQVDQANFSEVNTSPFELNSENVTKVSVLYNVTINNTYSC 252  
DB 162 LECTSGMVPBPQVQW--RTHRGEEPPSPMSSESRNPDEGLFTVRASVITIRDSMKNV-SC 218  
QY 253 MIENDIAKATGDIKVT 268  
DB 219 CIRNLLIGQKEVEVS 234  
  
RESULT 2  
BUTY\_HUMAN  
ID BUTY\_HUMAN STANDARD; PRT; 526 AA.  
AC Q13410;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Butyrophilin precursor (Bt) (Butyrophilin subfamily 1 member A1).  
GN BTNL1 OR BTN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast;  
RX MEDLINE=96201696; PubMed=8611614;  
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.,  
RT "Cloning and sequence analysis of human butyrophilin reveals a

RT potential receptor function".  
RL Biochim. Biophys. Acta 1306:1-4(1996).  
CC -!- FUNCTION: May function in the secretion of milk-fat droplets. It  
CC may act as a specific membrane-associated receptor for the  
CC association of cytoplasmic droplets with the apical plasma  
CC membrane (By similarity).  
CC -!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase  
CC (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG  
CC family.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.  
CC -----  
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CC -----  
DR EMBL; U39576; AAC50489.1; -  
DR PIR; S70587; S70587.  
DR Genew; HGNC:1135; BTNL1.  
DR MIM; 601610; -  
DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
DR GO; GO:0004872; F: receptor activity; TAS.  
DR InterPro; IPR001870; B302.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG V.  
DR InterPro; IPR006574; PRY.  
DR InterPro; IPR003877; SPRY\_receptor.  
DR Pfam; PF00047; IG; 1.  
DR Pfam; PF00622; SPRY; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00589; PRY; 1.  
DR SMART; SM00449; SPRY; 1.  
DR PROSITE; PS50835; IG-LIKE; 2.  
DR Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.  
KW SIGNAL  
FT CHAIN 1 26  
FT DOMAIN 27 526 BUTYROPHILIN.  
FT TRANSMEM 27 242 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 243 269 POTENTIAL.  
FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 27 138 IG-LIKE V-TYPE 1.  
FT DOMAIN 148 234 IG-LIKE V-TYPE 2.  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 526 AA; 59004 MW; E9CA0CF8DAF94D5 CRC64;  
  
Query Match 13.4%; Score 211.5; DB 1; Length 526;  
Best Local Similarity 26.6%; Pred. No. 2.6e-09;  
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;  
  
QY 75 IGEDGILSTFEEDIKLSDIVIQWLMKEGVLGVHFEKGEKDELSEODEMFRGRTAVFADQ 134  
DB 42 VGEDAELPCRLSPNVAKGMELRMFEKVPSPAVFVSREGQEGAEQWPEYRGRTAVQDG 101  
  
QY 135 VIVGNASLRKLVQTDAGTYKCYITTSKGNANLEYKTGAF-SMPEVNVYNASSE-T 192  
DB 102 IAGGSVAVRIQEKASDGEYCFPRDENTEEALVHLKVAALGSDPHISMVQESGEIC 161  
  
QY 193 LRCEAPRMFPQPTVWVASQVDQANFSEVNTSPFELNSENVTKVSVLYNVTINNTYSC 252  
DB 162 LECTSGMVPBPQVQW--RTHRGEEPPSPMSSESRNPDEGLFTVRASVITIRDTSTKQVSC 218  
QY 253 MIEN 256  
DB 219 YIQN 222  
  
RESULT 3  
BUTY\_MOUSE

ID BUTY\_MOUSE STANDARD; PRT; 524 AA.  
AC Q62556; P97392;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Butyrophilin precursor (Bt) (Butyrophilin subfamily 1 member A1).  
GN BTN1A1 OR BTN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Mammary gland;  
RX MEDLINE=97148936; PubMed=8995761;  
RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;  
RT "Structural organization and mammary-specific expression of the  
RT butyrophilin gene."  
RL Mamm. Genome 7:900-905 (1996).  
RN [2]  
RP SEQUENCE OF 39-487 FROM N.A.  
RC TISSUE=Mammary gland;  
RX MEDLINE=96125722; PubMed=8541302;  
RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;  
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin  
RT specifically associates with a 150-kDa protein of mammary epithelial  
RT cells and milk fat globule membrane."  
RL Biochim. Biophys. Acta 1245:285-292 (1995).  
CC -1- FUNCTION: May function in the secretion of milk-fat droplets. It  
CC may act as a specific membrane-associated receptor for the  
CC association of cytoplasmic droplets with the apical plasma  
CC membrane (By similarity).  
CC -1- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in  
CC association with the milk-fat-globule membrane during lactation.  
CC -1- DEVELOPMENTAL STAGE: Expression increases during the last half of  
CC pregnancy and is maximal during lactation.  
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG  
CC family.  
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.  
CC -----  
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CC -----  
DR EMBL; U67065; AAB51034.1; -.  
DR EMBL; S80642; AAB35893.1; -.  
DR MGI; MGI:103118; Bt1a1.  
DR InterPro; IPR001870; B302.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG v.  
DR InterPro; IPR006574; PRY.  
DR InterPro; IPR003877; SPRY\_receptor.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF00622; SPRY; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00589; PRY; 1.  
DR SMART; SM00449; SPRY; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.  
FT SIGNAL 1 26  
FT CHAIN 27 524  
FT DOMAIN 27 524 BUTYROPHILIN.  
FT TRANSMEM 248 268 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 269 524 POTENTIAL.  
FT DOMAIN 29 141 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 149 235 IG-LIKE V-TYPE 1.  
FT CARBOHYD 56 56 IG-LIKE V-TYPE 2.  
N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT FT 46 46 D -> DD (IN REF. 2).  
FT FT 117 117 V -> F (IN REF. 2).  
FT FT 191 191 E -> D (IN REF. 2).  
FT FT 210 210 R -> S (IN REF. 2).  
FT FT 363 363 V -> E (IN REF. 2).  
FT FT 408 408 T -> K (IN REF. 2).  
FT FT 413 413 SL -> FF (IN REF. 2).  
FT FT 420 423 PRV -> LAEY (IN REF. 2).  
FT FT 492 509 DIPSPLEGCTSGDKDT -> GHSLVAGRLYFWQRH  
FT FT (IN REF. 2).  
SQ SEQUENCE 524 AA; 58406 MW; 333F4DE2C7704480 CRC64;  
Query Match 11.3%; Score 178.5; DB 1; Length 524;  
Best Local Similarity 22.7%; Pred. No. 1.1e-06;  
Matches 45; Conservative 51; Mismatches 93; Indels 9; Gaps 4;  
QY 75 IGEDGILSCPEPDIKLSDIVIQMLKEGVGLVHEFKEDKLSQDEMFRGRFAVFDQ 134  
DB 43 VGSDAEITCGSPNASSEYVWELWPRQTRSTAVLLYRDQEQEQQMTYRGRATLATAG 102  
QY 135 VIVGNASLRKXVQLTDAGYKCYITTSKKGKNNLEKYGAF-SMEVNVVYNASSE-T 192  
DB 103 ILDGRATLLIRDVRSVDQGEYRCLEKNDPFEBAAYLVKVAAGSDPQSMVTQENGEME 162  
QY 193 LRCEAPRWFPQPTVWASQVDQGANFSEVSNT--SFEINSENVTKVVSVLXVNTINNTY 250  
DB 163 LECTSGWYFEPQVQWRT-----GNREMLPSTSSKKNHEEGFLTVAVSMIMDSISXKM 217  
QY 251 SCMIENDIAKATGDIKVT 268  
DB 218 SCCTQNTLLGQGEKEVIS 235  
RESULT 4  
CD80 RABIT STANDARD; PRT; 299 AA.  
AC P42070;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1  
DE antigen).  
GN CD80.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B/J X CHB:HM;  
RX MEDLINE=95369849; PubMed=7642234;  
RA Isono T., Seto A.;  
RT "Cloning and sequencing of the rabbit gene encoding T-cell  
RT costimulatory molecules."  
RL Immunogenetics 42:217-220 (1995).  
CC -1- FUNCTION: Involved in the costimulatory signal essential for T  
CC lymphocytes activation. T cell proliferation and cytokine  
CC production is induced by the binding of CD28 or CTLA-4 to this  
CC receptor.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -----  
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CC -----  
DR EMBL; D49843; BAA08643.1; -.





DB 53 ISPGKATGMEVGMVSPFSRVVHLRYNGKDQDAEAPERYGRTELKESIGKVALRI 112  
QY 145 KNVQLTDAGTYKCYITTSKGNANLEYK 173  
DB 113 QNVRFSDEGGYTCFPRDHSYOEAAVELK 141

RESULT 6  
MOG\_MOUSE  
ID MOG\_MOUSE STANDARD; PRT; 246 AA.  
AC Q61885; P70364; Q62003;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Myelin-oligodendrocyte glycoprotein precursor.  
GN MOG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10990;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=95130110; PubMed=7829100;  
RA Daubas P., Pham-Dinh D., Dautigny A.;  
RT "Structure and polymorphism of the mouse myelin/oligodendrocyte  
RL glycoprotein gene.";  
RN Genomics 23:36-41(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gardiner M.V., Mathieu J.M.;  
RT "Murine and human MOG are highly conserved: cDNA analysis";  
RL Trans. Am. Soc. Neurochem. 24:234-234(1993).  
RN [3]  
RP SEQUENCE OF 29-246 FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Brain;  
RX MEDLINE=93376728; PubMed=8367453;  
RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,  
RT Pontorotti P., Roeckel N., Mather I.H., Artzt K., Landahl K.F.,  
RN Dautigny A.;  
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the  
RL immunoglobulin superfamily encoded within the major  
RT histocompatibility complex.";  
RN Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).  
RN [4]  
RP SEQUENCE OF 29-54.  
RC STRAIN=BALB/c; TISSUE=Brain;  
RX MEDLINE=92218912; PubMed=1373175;  
RA Amiguet P., Gardiner M.V., Zanetta J.-P., Mathieu J.-M.;  
RT "Purification and partial structural and functional characterization  
RT of mouse myelin/oligodendrocyte glycoprotein.";  
RL J. Neurochem. 58:1676-1682(1992).  
CC -1- FUNCTION: Minor component of the myelin sheath. May be involved in  
CC completion and/or maintenance of the myelin sheath and in cell-  
CC cell communication.  
CC -1- SUBUNIT: May form homodimers.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Found exclusively in the CNS, where it is  
CC localized on the surface of myelin and oligodendrocyte cytoplasmic  
CC membranes.  
CC -1- DISEASE: Reduced concentrations of MOG are observed in jimpy and  
CC quacking dysmyelinating mutant mice.  
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. B2N/MOG  
CC family.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC -1- CAUTION: Do not confuse myelin-oligodendrocyte glycoprotein (MOG)  
CC with oligodendrocyte-myelin glycoprotein (OMG).  
CC -----  
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CC -----  
CC EMBL; L29503; AAC42023.1; -  
DR EMBL; L29498; AAC42023.1; JOINED.  
DR EMBL; L29500; AAC42023.1; JOINED.  
DR EMBL; L29501; AAC42023.1; JOINED.  
DR EMBL; L29499; AAC42023.1; JOINED.  
DR EMBL; L29502; AAC42023.1; JOINED.  
DR EMBL; U64572; AAB08096.1; -  
DR EMBL; L20942; AAA03180.1; -  
DR PIR; A55717; A55717.  
DR MGD; MGI:97435; Mog.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV\_1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KM Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.  
FT SIGNAL 1 28  
FT CHAIN 1 28  
FT DOMAIN 29 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.  
FT TRANSMEM 157 177 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 178 209 POTENTIAL.  
FT TRANSMEM 210 230 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 211 246 POTENTIAL.  
FT DOMAIN 31 144 IG-LIKE V-TYPE.  
FT DISULFID 52 126 POTENTIAL.  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. ) (POTENTIAL).  
FT CONFLICT 21 21 L -> LL (IN REF. 2).  
FT CONFLICT 32 32 R -> G (IN REF. 4).  
FT CONFLICT 95 95 G -> E (IN REF. 3).  
FT CONFLICT 169 169 P -> S (IN REF. 2).  
SQ SEQUENCE 246 AA; 28271 MW; 1F1A84A40D5CFB89 CRC64;

Query Match 9.6%; Score 150.5; DB 1; Length 246;  
Best Local Similarity 23.8%; Pred. No. 7e-05;  
Matches 34; Conservative 33; Mismatches 65; Indels 11; Gaps 2;  
QY 37 MS-----ISITITLGAIALITGFGISGRHSITVTIVASAGNIGEGILSTCFEPDIK 90  
DB 5 WFSWSPSCFSLTLH-----LQSCSYAGQFRVIGPGVPIRALVGDALPGRISPGKN 59  
QY 91 LSDIVIQWLKEGVIGLVHEFEKEDLESDQDEMFRGRTAVFADQVIVGNASRLKNVQLT 150  
DB 60 ATGMEVGMVSPFSRVVHLRYNGKDQDAEAPERYGRTELKESIGKVALRIQVRF 119  
QY 151 DAGTYKCYITTSKGNANLEYK 173  
DB 120 DEGGYTCFPRDHSYOEAAVELK 142

RESULT 7  
ICOL\_HUMAN  
ID ICOL\_HUMAN STANDARD; PRT; 302 AA.  
AC Q75144; Q9HD18; Q9NR01;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GI50)  
DE (B7-related protein-1) (B7RP-1).  
GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Dendritic cell;  
RX MEDLINE=20477846; PubMed=11023515;  
RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;  
RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds  
RT ICOS.";

```

RL Blood 96:2808-2813 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=20465019; PubMed=11007762;
RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT "Characterization of a new human B7-related protein: B7RP-1 is the
RT ligand to the co-stimulatory protein ICOS.";
RL Int. Immunol. 12:1439-1447 (2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finerly H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zoliner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RL J. Immunol. 164:1653-1657 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kohani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176 (1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Ling V., Dunnisi-Joannopoulos K.;
RT "GL50 molecules and uses therefor.";
RL Patent number WO0121796, 29-MAR-2001.
CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=O75144-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O75144-2; Sequence=VSP_002520;
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
CC LYMPH NODES, LEUKOCYTES AND SPLEEN.
CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
CC family.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300
CC onward for an unknown reason.
CC -----
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CC -----
DR EMBL; AF199028; AAF34739.1; -.
DR EMBL; AF289028; AAG01176.1; -.
DR EMBL; AF216749; AAK16241.1; -.
DR EMBL; AB014553; BAA31628.1; ALT_SEQ.
DR EMBL; AX100595; CAC36465.1; -.
DR MIM; 605717; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; TAS.
DR GO; GO:0007165; P:signal transduction; NAS.
DR GO; GO:0042110; P:T-cell activation; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR PROSITE; PS50835; Ig_LIKE; 2.
KW B-cell activation; Immune response; Glycoprotein;
KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 302
FT DOMAIN 19 256
FT TRANSMEM 257 277
FT DOMAIN 278 302
FT DOMAIN 19 129
FT DOMAIN 141 227
FT DISULFID 37 113
FT DISULFID 158 216
FT CARBOHYD 70 70
FT CARBOHYD 137 137
FT CARBOHYD 173 173
FT CARBOHYD 186 186
FT CARBOHYD 225 225
FT VARSPIC 300 302
FT FTID=VSP_002520.
SQ SEQUENCE 302 AA; 33349 MW; 647934E21B55E34A CRC64;
Query Match 9.4%; Score 147.5; DB 1; Length 302;
Best Local Similarity 24.5%; Pred. No. 0.00016;
Matches 66; Conservative 41; Mismatches 117; Indels 45; Gaps 13;
QY 75 IGEDGLISTCTEPPD--IKSDIVYQWLKRGVGLVHEKEGDELSEDEMRGRTRVAF 131
DB 29 VGSDEVELSCAC-PEGSRFDLNDVYVYQWSESKTVYTHIPQNSSLNVDSPYRNRLAMS 87
QY 132 ADVQIVGNASRLKLVQLTAGTYCYITTSKKG-----NANLEYKTGA-PSMEPVAVD 185
DB 88 PAGMLRGDFSLRLFNVTPODEQKPHC-LVLSQSLGFQEVLSVEVTLHYAANFSPVVSAP 146
QY 186 YNASSS--TLRCEAPRFWPOPTVVAASQVQGANFSEVNTSPELNSENVTKVSVLYN 243
DB 147 HSPSQBELTFTCTSLNGYPRPNVYINKTDNSLDDALONDTVFLNKGGL-YDVVSVLRI 205
QY 244 V-TINNTYSCMIEN-----DIKATG-DI---KVTSEI-----KRSHLQLNSKAS 286
DB 206 APTPSVNIQCIENLVLLQNLTVGSQGTGNDIGERDKITENPVSTGEKNAATWSILAVICL 265
QY 287 L-----CVSSFFAISWALLP 301
DB 266 LVVVAVAIGWVCRDRLCHSHVAGMAVSP 294
RESULT 8
CD86_HUMAN STANDARD; PRT; 329 AA.
AC P42081; Q13655;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
antigen) (CTLA-4 counter-receptor B7.2) (B70) (FBN-1) (BUE3).

```

GN CD86 OR CD28LG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=94053735; PubMed=7694363;  
RA Freeman G.J., Gribben J.G., Bousquet V.A., Ng J.W.,  
RA Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;  
RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T  
RL cell proliferation.";  
RL Science 262:909-911(1993).  
RN [2]  
RP SEQUENCE OF 7-329 FROM N.A.  
RX MEDLINE=94050123; PubMed=7694153;  
RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,  
RA Lanier L.L., Somoza C.;  
RT "B70 antigen is a second ligand for CTLA-4 and CD28.";  
RL Nature 366:76-79(1993).  
RN [3]  
RP SEQUENCE OF 7-329 FROM N.A.  
RX TISSUE=Forebrain;  
RX MEDLINE=95331831; PubMed=7541777;  
RA Jellis C.L., Mang S.S., Rennett P., Borriello F., Sharpe A.H.,  
RA Green N.R., Gray G.S.;  
RT "Genomic organization of the gene coding for the costimulatory human  
RL B-lymphocyte antigen B7-2 (CD86).";  
RL Immunogenetics 42:85-89(1995).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=95088403; PubMed=7527824;  
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,  
RA Okumura K., Ito D., Azuma M.;  
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T  
RL cell proliferation, cytokine production, and generation of CTL.";  
RL J. Immunol. 154:97-105(1995).  
RN [5]  
RP IDENTIFICATION AS CD86.  
RX MEDLINE=94348060; PubMed=7520767;  
RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,  
RA Nadler L.M., Wakasa H., Tedder T.F.;  
RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and  
RL activated B lymphocytes is the CD86 differentiation antigen.";  
RL Blood 84:1402-1407(1994).  
CC - FUNCTION: Receptor involved in the costimulatory signal essential  
CC for T lymphocyte proliferation and interleukin 2 production, by  
CC binding CD28 or CTLA-4. May play a critical role in the early  
CC events of T cell activation and costimulation of naive T cells,  
CC such as deciding between immunity and energy that is made by T  
CC cells within 24 hours after activation.  
CC - SUBCELLULAR LOCATION: Type I membrane protein.  
CC - TISSUE SPECIFICITY: Expressed by activated B lymphocytes and  
CC monocytes.  
CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC - SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
CC - DATABASE: NAME=PROT; NOTE=CD guide CD86 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/ncbi/cd/cd86.htm".  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; L25259; AAA58389.1; -;  
DR EMBL; U04343; AAB03814.1; -;  
DR EMBL; U17722; AAA86473.1; -;  
DR EMBL; U17717; AAA86473.1; JOINED.  
DR EMBL; U17718; AAA86473.1; JOINED.  
DR EMBL; U17719; AAA86473.1; JOINED.

DR EMBL; U17721; AAA86473.1; JOINED.  
DR PIR; A48754; A48754.  
DR PDB; 1I85; 04-APR-01.  
DR Genew; HGNC:11705; CD86.  
DR MIM; 601020; -;  
DR GO; GO:0004872; F:receptor activity; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
DR PROSITE; PS00290; IG\_MHC; FALSE NEG.  
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
KW Receptor; Polymorphism; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 329  
FT DOMAIN 24 247  
FT TRANSMEM 248 268  
FT DOMAIN 269 329  
FT DOMAIN 33 131  
FT DOMAIN 150 225  
FT DISULFID 40 110  
FT DISULFID 157 218  
FT CARBOHYD 33 33  
FT CARBOHYD 47 47  
FT CARBOHYD 135 135  
FT CARBOHYD 146 146  
FT CARBOHYD 154 154  
FT CARBOHYD 177 177  
FT CARBOHYD 192 192  
FT CARBOHYD 213 213  
FT VARIANT 310 310  
FT CONFLICT 27 27  
FT FTID=VAR 014650.  
SQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;  
Query Match 9.4%; Score 147.5; DB 1; Length 329;  
Best Local Similarity 23.4%; Pred. No. 0.00018;  
Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;  
QY 50 IALLIGIGISGRHSIVTVTVASAGNIGEDGLSCFF--EPDIKSDIVIOMLKEGVLGIV 107  
DB 12 ILFVMAFLSLGAPLKIQAY-----FNETADLPQCFANSQNSISELVFWQDENT--VL 65  
QY 108 HEFEKGEDELSEQDENFRGRTAVPDDQVIYGNASIRLKNVQLTDAGTYKCYIITSKKG- 166  
DB 66 NEVYLIGKEKFPVSHSKYMGRTSFDSD-----SWLRLNHLQIKKGLVQCIHHKKPTGM 120  
QY 167 ---NANLEKYTKGA-FSMPEV---NVDYNASSETLRCEAPRMFQPTVWASQVDQGAN 217  
DB 121 ITHQNMSELSTVLANSFQPEIVPISNITENVYI-NLTGSIHGIRPEP----- 166  
QY 218 FEEVSNSTFEINSENVTKV-----VSVLYNVTI-----NNTYSCEMEN 256  
DB 167 ---KKNSVLIRTKNSTIEYDGIOMKQSQDNVTELDVDSISLSVSPEDVTSNMTIFCILET 222  
QY 257 DIAKATDIXTSESIKR--RSHLQLINS---KASLGVSSFFALSM 297  
DB 223 DTRLLSSPFSFIELEDPQPPDPHPIWITAVLPVTIICVWVFCILIM 268  
RESULT 9  
CD86\_RABIT  
ID CD86\_RABIT STANDARD; PRT; 330 AA.  
AC P42071;  
DT 01-NOV-1995 (Rel. 32; Created)  
DT 01-NOV-1995 (Rel. 32; Last sequence update)  
DT 10-OCT-2003 (Rel. 42; Last annotation update)  
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2  
DE antigen).  
GN CD86.

```

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OK NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B/J X CHB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules."
RT Immunogenetics 42:217-220(1995).
RL -1- FUNCTION: Receptor involved in the costimulatory signal essential
CC for T lymphocyte proliferation and interleukin 2 production, by
CC binding CD28 or CTLA-4. May play a critical role in the early
CC events of T cell activation and costimulation of naive T cells,
CC such as deciding between immunity and anergy that is made by T
CC cells within 24 hours after activation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; D49842; BAA08642.1; -.
DR PIR; I46691; I46691.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 127 IG-LIKE V-TYPE.
FT DOMAIN 150 225 IG-LIKE C2-TYPE.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA; 37142 MW; 935CD65C57E3BE1 CRC64;

Query Match 9.4%; Score 147.5; DB 1; Length 330;
Best Local Similarity 24.0%; Pred. No. 0.00018;
Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;

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DB 109 QCFVHHGAKGLVPIYQMSLSVLANFTQPEITLISNTRNSAINLTCSSVQGYEPBK 168
QY 207 VVASQVDQGANFSEVNSNTSELSNNVTKV-----VSVLVNTTINNTYSCMIEN 256
DB 169 MF-----FVLKTEENATEYDGVIEKSDQNVGLNINISISG--SITPSD 209
QY 257 DIKAT 262
DB 210 DIRNAT 215

RESULT 10
MOG_HUMAN STANDARD; PRT: 247 AA.
ID MOG_HUMAN
AC Q16653; O00713; O00714; O00715; Q13054; Q13055; Q14855; Q92891;
AC Q92892; Q92893; Q92894; Q92895; Q93053; Q96KU9; Q96KV0; Q99605;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-oligodendrocyte glycoprotein precursor.
GN MOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=95310943; PubMed=7790876;
RA Hilton A.A., Slavin A.J., Hilton D.J., Bernard C.C.A.;
RT "Characterization of cDNA and genomic clones encoding human myelin
RT oligodendrocyte glycoprotein."
RT J. Neurochem. 65:309-318(1995).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95054056; PubMed=7964757;
RA Pham-Dinh D., Allingant B., Ruberg M., della Gaspera B.,
RA Nussbaum J.-L., Dautigny A.;
RT "Characterization and expression of the cDNA coding for the human
RT myelin/oligodendrocyte glycoprotein."
RT J. Neurochem. 63:2353-2356(1994).
RL [3]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96015053; PubMed=8530032;
RA Roth M.-P., Malfroy L., Offer C., Sevin J., Enault G., Borot N.,
RA Pontarotti P., Coppin H.;
RT "The human myelin oligodendrocyte glycoprotein (MOG) gene: complete
RT nucleotide sequence and structural characterization."
RL Genomics 28:241-250(1995).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96115584; PubMed=8666381;
RA Pham-Dinh D., della Gaspera B., de Rosbo N.K., Dautigny A.;
RT "Structure of the human myelin/oligodendrocyte glycoprotein gene and
RT multiple alternative spliced isoforms."
RL Genomics 29:345-352(1995).
RN [5]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Balentine P.A., Gardiner M.V.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 5 AND 7).
RA Griffiths C.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP STRUCTURE BY NMR OF 64-84.
RX MEDLINE=97354172; PubMed=9210466;
RA Albour-Abo S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
RT "A conformational study of the human and rat encephalitogenic myelin
RT oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
CC -1- FUNCTION: Minor component of the myelin sheath. May be involved in
CC completion and/or maintenance of the myelin sheath and in cell-

```

CC cell communication.  
 CC -1- SUBUNIT: May form homo- or heterodimers between the different  
 CC isoforms.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (isoforms 1 and  
 CC 5); type I membrane protein (other isoforms) (Potential).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=9;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1; Synonyms=Alpha-1;  
 CC IsoId=Q16653-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Alpha-2;  
 CC IsoId=Q16653-2; Sequence=VSP\_002543;  
 CC Name=3; Synonyms=Alpha-3;  
 CC IsoId=Q16653-3; Sequence=VSP\_002542;  
 CC Name=4; Synonyms=Alpha-4;  
 CC IsoId=Q16653-4; Sequence=VSP\_002539;  
 CC Name=5; Synonyms=Beta-1;  
 CC IsoId=Q16653-5; Sequence=VSP\_002545;  
 CC Name=6; Synonyms=Beta-2;  
 CC IsoId=Q16653-6; Sequence=VSP\_002543;  
 CC Name=7; Synonyms=Beta-3;  
 CC IsoId=Q16653-7; Sequence=VSP\_002545;  
 CC Name=8; Synonyms=Beta-4;  
 CC IsoId=Q16653-8; Sequence=VSP\_002544;  
 CC Name=9;  
 CC IsoId=Q16653-9; Sequence=VSP\_002540, VSP\_002541;  
 CC Note=Not functionally active. May be expressed at low level in  
 CC the adult;  
 CC -1- TISSUE SPECIFICITY: Found exclusively in the CNS, where it is  
 CC localized on the surface of myelin and oligodendrocyte cytoplasmic  
 CC membranes.  
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. EBN/MOG  
 CC family.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -1- CAUTION: Do not confuse myelin oligodendrocyte glycoprotein (MOG)  
 CC with oligodendrocyte-myelin glycoprotein (OMG).  
 CC  
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 CC  
 CC -----  
 CC EMBL; X74511; CA52617.1; -  
 CC EMBL; Z48051; CA88109.1; -  
 CC EMBL; U18840; AAC50361.1; -  
 CC EMBL; U18843; AAC50362.1; -  
 CC EMBL; U18798; AAC50876.1; -  
 CC EMBL; U18799; AAC50877.1; -  
 CC EMBL; U18800; AAC36870.1; -  
 CC EMBL; U18801; AAC50878.1; -  
 CC EMBL; U18803; AAC50879.1; -  
 CC EMBL; U64564; AAB08088.1; -  
 CC EMBL; U64565; AAB08089.1; -  
 CC EMBL; U64566; AAB08090.1; -  
 CC EMBL; U64567; AAB08091.1; -  
 CC EMBL; U64568; AAB08092.1; -  
 CC EMBL; U64569; AAB08093.1; -  
 CC EMBL; U64570; AAB08094.1; -  
 CC EMBL; U64571; AAB08095.1; ALT\_SEQ.  
 CC EMBL; AL050328; CAB89267.1; -  
 CC EMBL; AL050328; CAB89269.1; -  
 CC EMBL; AL050328; CAB89270.1; -  
 CC EMBL; AL050328; CAB89271.1; -  
 CC Genew; HGNC:7157; MOG.  
 CC MIM; 159465; -  
 CC GO; GO:0007417; P:central nervous system development; TAS.  
 CC InterPro; IPR007110; Ig-like.  
 CC Pfam; PF00047; Ig\_1.  
 CC PROSITE; PS50835; IG\_LIKE; 1.  
 CC Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal;  
 KW

KW Alternative splicing.  
 FT SIGNAL 1 29  
 FT CHAIN 30 247  
 FT DOMAIN 30 154  
 FT TRANSMEM 155 175  
 FT DOMAIN 176 210  
 FT TRANSMEM 211 231  
 FT DOMAIN 232 247  
 FT DOMAIN 32 145  
 FT DISULFID 53 127  
 FT CARBOHYD 60 60  
 FT VARSPPLIC 30 145  
 FT VARSPPLIC 198 203  
 FT VARSPPLIC 204 247  
 FT VARSPPLIC 198 236  
 FT VARSPPLIC 198 236  
 FT VARSPPLIC 198 243  
 FT VARSPPLIC 244 247  
 FT VARSPPLIC 244 247  
 FT CONFLICT 171 171  
 FT SEQUENCE 247 AA; 28179 MW; 847601FE5997AB0C CRC64;  
 V -> L (IN REF. 3).  
 Query Match 9.1%; Score 144; DB 1; Length 247;  
 Best Local Similarity 20.8%; Pred. No. 0.00023;  
 Matches 49; Conservative 39; Mismatches 80; Indels 68; Gaps 6;  
 QY 28 MASLQILFMSIISIIIL-----AGATALLIGFSGHSHITVTVAAGNIGED 78  
 DB 1 MASLSPSPSCLSFLILLVSSSYAGQPRV-----IGPHPIAL-----VGDE 48  
 QY 79 GILCTFEPDIKLSDIVIOWLKEGVGLGHEFEKGEKDELSEDEMFGRTAVFADQVIVG 138  
 DB 49 VELPERISPKNAAGMEVGYRPPFSRYVHLVNRNGKQDDGDAPERYGRTEILKDAIGEG 108  
 QY 139 NASLELKNVQLTDAGTYKCIITISKGNANLEYKTGAFSMEVNVVNASSETLRCEAP 198  
 DB 109 KVTLLIRINRVFSDGEGFTCFEFDHDSYGEAAAE-----LKVEDP 147  
 QY 199 RWFPOPTVWASQVDQANFSEVSNISPELSENVTMKVSV-LYNTTINTNTYSCM 253  
 DB 148 FYWVSPGVL-----VLAVALPVLLQITGVAVFLCL 178  
 RESULT 11  
 CD86\_MOUSE STANDARD; PRT; 309 AA.  
 ID CD86\_MOUSE  
 AC P42082;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE T lymphocyte activation antigen CD86 precursor (Activation B7-2  
 DE antigen) (Early T cell costimulatory molecule-1) (ERC-1).  
 GN CD86.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94065585; PubMed=7504059;  
 RA Freeman G.J., Bortello F., Hodés R.J., Reiser H., Gribben J.G.,  
 RA Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,  
 RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;  
 RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates





```

CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
CC family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- CAUTION: Do not confuse myelin-oligodendrocyte glycoprotein (MOG)
CC with oligodendrocyte-myelin glycoprotein (OMG).
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CC -----
DR EMBL; L21757; -; NOT_ANNOTATED_CDS.
DR PIR; A47712; A47712.
DR HSSP; Q13740; 1KUC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig, 1.
DR SMART; SM00406; Ig, 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
FT SIGNAL 1 28
FT CHAIN 29 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
FT DOMAIN 29 153 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 154 174 POTENTIAL.
FT DOMAIN 175 209 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 210 230 POTENTIAL.
FT DOMAIN 231 246 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 29 144 IG-LIKE V-TYPE.
FT DISULFID 52 126 POTENTIAL.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 246 AA; 28028 MW; 363C76ABA33DE41 CRC64;

Query Match 8.9%; Score 140.5; DB 1; Length 246;
Best Local Similarity 26.1%; Pred.No. 0.00044;
Matches 31; Conservative 25; Mismatches 50; Indels 13; Gaps 1;

QY 68 TVASAGN-----IGEDGILSCTEPEPDIKSLDIVIOMLKEGYLGLVHEFKGK 114
DB 24 TSSSAGQFRVIGPGHPIRALVGEVDEYELPCRISPGKNATGMEGVYRPPFSRVVHLYRNGK 83
QY 115 DELSEODEMFRGRTAVFADQYIVGNASLRKNVQLTDAGYKCVITITSGKGNANLEVK 173
DB 84 DQDEQAPRYKGRTOLEKRTIGEGKVTLRIRNVRSDEGFTCFRDSYGEAEAMELK 142

RESULT 13
NCA2 HUMAN STANDARD; PRT; 761 AA.
ID P13592; P13593;
AC 01-JAN-1990 (Rel. 13, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
DE (NCAM-120) (CD56 antigen).
GN NCAM1 OR NCAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN 11
RP SEQUENCE FROM N.A. (ISOFORM N-CAM 120).
RX MEDLINE=89305258; PubMed=3253057;
RA Barton C.H., Dickson G., Gower H.J., Rowett L.H., Putt W.,
RA Elsom V., Moore S.E., Goridis C., Walsh F.S.;
RT "Complete sequence and in vitro expression of a tissue-specific
RT phosphatidylinositol-linked N-CAM isoform from skeletal muscle.";
RL Development 104:165-173 (1988).
RN 12
RP SEQUENCE OF 491-761 FROM N.A. (ISOFORM N-CAM 120).

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RC TISSUE=Skeletal muscle;
RX MEDLINE=87301755; PubMed=2887295;
RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
RA Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
RT "Human muscle neural cell adhesion molecule (N-CAM): identification
RT of a muscle-specific sequence in the extracellular domain.";
RL Cell 50:1119-1130 (1987).
RN 13
RP SEQUENCE OF 491-655 FROM N.A. (ISOFORM C).
RX MEDLINE=89077552; PubMed=3203385;
RA Gower H.J., Barton C.H., Elsom V.L., Thompson J., Moore S.E.,
RA Dickson G., Walsh F.S.;
RT "Alternative splicing generates a secreted form of N-CAM in muscle
RT and brain.";
RL Cell 55:955-964 (1988).
CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC neurites, etc.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=N-CAM 120;
CC IsoId=P13592-2; Sequence=Displayed;
CC Name=N-CAM 140;
CC IsoId=P13591-1; Sequence=External;
CC Name=C; Synonyms=Secreted;
CC IsoId=P13592-1; Sequence=VSP_002587;
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD56 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd56.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X16841; CAA34739.1; -
DR EMBL; M17409; AAA59912.1; -
DR EMBL; M22094; AAA59910.1; -
DR EMBL; M22092; AAA59911.1; -
DR EMBL; M22091; AAA59911.1; JOINED.
DR PIR; A31635; A31635.
DR PIR; S07784; ITHUNG.
DR Genew; HGNC:7656; NCAM1.
DR MIM; 116930; -
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
KW GPI-anchor; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 761
FT DOMAIN 20 111 NEURAL CELL ADHESION MOLECULE 1, 120 kDa
FT DOMAIN 116 205 IG-LIKE C2-TYPE 1.
FT DOMAIN 212 301 IG-LIKE C2-TYPE 2.
FT DOMAIN 308 403 IG-LIKE C2-TYPE 3.
FT DOMAIN 406 491 IG-LIKE C2-TYPE 4.
FT DOMAIN 518 595 IG-LIKE C2-TYPE 5.
FT DOMAIN 660 727 FIBRONECTIN TYPE-III 1.
FT DISULFID 41 96 FIBRONECTIN TYPE-III 2.
PROBABLE.

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FT CONFLICT 239 239 G -> R (IN REF. 2).
FT CONFLICT 490 490 L -> F (IN REF. 2).
FT CONFLICT 599 600 OG -> R (IN REF. 3).
FT CONFLICT 720 721 MISSING (IN REF. 3).
FT CONFLICT 811 811 G -> A (IN REF. 3).
SQ SEQUENCE 848 AA; 93360 MW; 68D2F0C0E6C1C2AD CRC64;

Query Match 8.6%; Score 135; DB 1; Length 848;
Best Local Similarity 23.2%; Pred. No. 0.0059;
Matches 64; Conservative 49; Mismatches 111; Indels 52; Gaps 13;

QY 63 SITVTVASAGNIGEDGILSCFP-----EPDIKLSDIVIQLMEGLVGLVHEFEKQDE 116
Db 77 SSTLTITVNA-NIDDAGIKCVVTGEGDSESEATVNVKIFQKMFKNAPPTQEFREGEDA 135
QY 117 LSEQDEM-----FRGRTAVFADQY---IVGNASLRLKXVQLTDAGTYKCYITSK 163
Db 136 VIVCDVSSLPPTIIMKRGKDVILKKDVRPVLNNYLIQIRGIKTDGTYRC-----E 190
QY 164 G---KGNANLEYKTGAFSME-----VNVDTN-ASSETLRCEAPRPFPQPTVWAS 210
Db 191 GRLARGEINFQIVIVNVPTTIOARQNTVNTANLGGSVTLVCD-EGFEPPTMSWTX 249
QY 211 QVDQGANFSEVNTSEFELNSENVTKVSVLYNTVNTNTYSCMIENDIAK--ATGDIKYT 268
Db 250 DGEQIREBEDDEKITSDDSGQLTKV----DKXDEAYITCIAENKAGEQDATHLKVF 305
QY 269 E---SEIKRRSHLQLNSKASLCVSS---FFAISM 297
Db 306 AKPKITYENQJAMELEBQVTLTCBASGDPIPSITW 341

RESULT 15
SHS1_HUMAN STANDARD; PRT: 503 AA.
AC P78324; O00683; O43799; Q8N517; Q8TAL8; Q9H0Z2; Q9UDX2; Q9UII6;
AC Q9Y4U9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHPs-1) (inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (SIRP-alpha-1) (SIRP-alpha-2) (SIRP-alpha-
DE 3) (MYD-1 antigen) (Brain Ig-L1 molecule with tyrosine-based
DE activation motifs) (Bit) (Macrophage fusion receptor) (p84).
GN PTPN61 OR SHPS1 OR SIRP OR MYD1 OR BIT OR MFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=97223399; PubMed=9070220;
RA Yamao T., Matosaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,
RA Fujioka Y., Kasuga M.;
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT localization of genes.";
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), POLYMORPHISM, PHOSPHORYLATION,
RP N-GLYCOSYLATION, AND INTERACTIONS WITH PTPN11, PTPN6 AND GRB2.
RC TISSUE=Placenta;
RX MEDLINE=97215901; PubMed=9062191;
RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
RA Ulrich A.;
RT "A family of proteins that inhibit signalling through tyrosine kinase
RT receptors.";
RL Nature 386:181-186(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND VARIANTS ASP-95; LEU-96; ASN-100;
RP ARG-107; GLY-109 AND VAL-131.
RC TISSUE=Monocytes;

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RX MEDLINE=98143722; PubMed=9485180;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells.";
RL Eur. J. Immunol. 28:1-11(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-44; THR-50; THR-52;
RP ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107; GLY-109 AND
RP VAL-131.
RC TISSUE=Brain;
RX MEDLINE=20053880; PubMed=10585853;
RA Sano S.-I., Ohnishi H., Kubota M.;
RT "Gene structure of mouse BIT/SHPS-1.";
RL Biochem. J. 344:667-675(1999).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beate D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Brideman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivasialho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin R., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitcaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; THR-50;
RP THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-107;
RP GLY-109 AND VAL-131.
RC TISSUE=Brain, Kidney, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]

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RP FUNCTION, AND INTERACTIONS WITH FYB; SCAP2 AND PTK2B.  
RX MEDLINE=99401000; PubMed=10469599;  
RA Timsa J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,  
RA Schraven B., Neel B.G.;  
RT "SHPS-1 is a scaffold for assembling distinct adhesion-regulated  
RT multi-protein complexes in macrophages.";  
RL Curr. Biol. 9:927-930(1999).  
[8]  
RN PHOSPHORYLATION BY JAK2, AND INTERACTIONS WITH PTPN11 AND JAK2.  
RX MEDLINE=20428742; PubMed=10842184;  
RA Stoege M.R., Argentsinger L.S., Wang H., Ullrich A., Carter-Su C.;  
RT "Negative regulation of growth hormone receptor/JAK2 signaling by  
RL signal regulatory protein alpha.";  
J. Biol. Chem. 275:28222-28229(2000).  
[9]  
RP FUNCTION, AND INTERACTION WITH CD47.  
RX MEDLINE=21400825; PubMed=11509594;  
RA Latour S., Tanaka H., Demeure C., Mateo V., Rubio M., Brown E.J.,  
RA Maliszewski C., Lindberg F.P., Oldenborg A., Ullrich A.,  
RA Delapasse G., Sarfati M.;  
RT "Bidirectional negative regulation of human T and dendritic cells by  
RT CD47 and its cognate receptor signal-regulator protein-alpha:  
RT down-regulation of IL-12 responsiveness and inhibition of dendritic  
RT cell activation";  
J. Immunol. 167:2547-2554(2001).

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OM protein - protein search, using sw model

Run on:

May 11, 2004, 16:23:01 ; Search time 47 Seconds  
(without alignments)  
1824.854 Million cell updates/sec

Title: US-09-827-271-392

Perfect score: 1574  
Sequence: 1 HASAHASGRORQHLSASTQI.....SSEFAISWALLPLSPYIMLK 309

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications RA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/ECT\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1574	100.0	309	9	US-09-778-320-209
2	1574	100.0	309	9	US-09-910-689-209
3	1574	100.0	309	9	US-09-884-441-392
4	1574	100.0	309	10	US-09-907-969-392
5	1574	100.0	309	10	US-09-827-271-392
6	1574	100.0	309	13	US-10-010-742-209
7	1574	100.0	309	14	US-10-198-053-392
8	1431	90.9	282	9	US-09-778-320-208
9	1431	90.9	282	9	US-09-850-178-33
10	1431	90.9	282	9	US-09-877-065-8
11	1431	90.9	282	9	US-09-989-722-291
12	1431	90.9	282	9	US-09-989-723-291
13	1431	90.9	282	9	US-09-989-279-291
14	1431	90.9	282	9	US-09-989-727-291
15	1431	90.9	282	9	US-09-910-689-208

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17	1431	90.9	282	9	US-09-884-441-393	Sequence 393, App
18	1431	90.9	282	9	US-09-889-732-291	Sequence 291, App
19	1431	90.9	282	9	US-09-991-073-291	Sequence 291, App
20	1431	90.9	282	9	US-09-990-442-291	Sequence 291, App
21	1431	90.9	282	9	US-09-991-163-291	Sequence 291, App
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26	1431	90.9	282	9	US-09-896-738-2	Sequence 2, Appli
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38	1431	90.9	282	10	US-09-997-428-291	Sequence 291, App
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44	1431	90.9	282	10	US-09-998-156-291	Sequence 291, App
45	1431	90.9	282	10	US-09-990-437-291	Sequence 291, App

#### ALIGNMENTS

RESULT 1  
US-09-778-320-209  
Sequence 209, Application US/09778320  
Patent No. US20010034052A1  
GENERAL INFORMATION:  
APPLICANT: Dillon, Davin C.  
APPLICANT: Day, Craig H.  
APPLICANT: Jiang, Yugui  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Mitcham, Jennifer  
APPLICANT: Wang, TongTong  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: DIAGNOSIS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.491C5  
CURRENT APPLICATION NUMBER: US/09/778,320  
CURRENT FILING DATE: 2001-02-06  
NUMBER OF SEQ ID NOS: 301  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 209  
LENGTH: 309  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-778-320-209

Query Match 100.0%; Score 1574; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 6.5e-138;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRORQHLSASTQIRWEPSPMASIGQILFWISIIIIIIAGATALLIGFISG 60  
DB 1 HASAHASGRORQHLSASTQIRWEPSPMASIGQILFWISIIIIIIAGATALLIGFISG 60  
QY RHSTITVTVAAGNIGEDGIICTFEPDIKLSDIVIQLKGVGLGVHFEKSGKDELSEQ 120  
DB RHSTITVTVAAGNIGEDGIICTFEPDIKLSDIVIQLKGVGLGVHFEKSGKDELSEQ 120  
QY 121 DEMERGRATVAFADQVIVGNASIRLKNVQLTDAGTYKCYIIITSGKGNANIEYKTAFAFMP 180



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Db      121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP 180
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Db      181 EVNVVDYNASSELRCEAPRPFQPTVWASQVDQANFSEVSNTSFEINSENVTKVSV 240
QY      241 LYNVTINNNTSCMIENDIAKATGDIKVTSEIKRSHLOLNSKASLCVSSFFAISWALL 300
Db      241 LYNVTINNNTSCMIENDIAKATGDIKVTSEIKRSHLOLNSKASLCVSSFFAISWALL 300
QY      301 PLSPYIMLK 309
Db      301 PLSPYIMLK 309
```

## RESULT 2

```
US-09-910-689-209
; Sequence 209, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; NUMBER OF SEQ ID NOS: 2001-07-20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-689-209
```

```
Query Match      100.0%; Score 1574; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HASAHASGRORQHSASTQIRWEPSPAMASLGQILFWSIIISIIIIAGAIALLIGFISG 60
Db      1 HASAHASGRORQHSASTQIRWEPSPAMASLGQILFWSIIISIIIIAGAIALLIGFISG 60
QY      61 RHSITVTVASAGNIGEDGILSCFEPDIKLSIVIQWLKEGVLGVHEFKEGKDEISEQ 120
Db      61 RHSITVTVASAGNIGEDGILSCFEPDIKLSIVIQWLKEGVLGVHEFKEGKDEISEQ 120
QY      121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP 180
Db      121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP 180
QY      181 EVNVVDYNASSELRCEAPRPFQPTVWASQVDQANFSEVSNTSFEINSENVTKVSV 240
Db      181 EVNVVDYNASSELRCEAPRPFQPTVWASQVDQANFSEVSNTSFEINSENVTKVSV 240
QY      241 LYNVTINNNTSCMIENDIAKATGDIKVTSEIKRSHLOLNSKASLCVSSFFAISWALL 300
Db      241 LYNVTINNNTSCMIENDIAKATGDIKVTSEIKRSHLOLNSKASLCVSSFFAISWALL 300
QY      301 PLSPYIMLK 309
Db      301 PLSPYIMLK 309
```

## RESULT 3

US-09-884-441-392

```
; Sequence 392, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 2001-06-18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 392
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-392
```

```
Query Match      100.0%; Score 1574; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HASAHASGRORQHSASTQIRWEPSPAMASLGQILFWSIIISIIIIAGAIALLIGFISG 60
Db      1 HASAHASGRORQHSASTQIRWEPSPAMASLGQILFWSIIISIIIIAGAIALLIGFISG 60
QY      61 RHSITVTVASAGNIGEDGILSCFEPDIKLSIVIQWLKEGVLGVHEFKEGKDEISEQ 120
Db      61 RHSITVTVASAGNIGEDGILSCFEPDIKLSIVIQWLKEGVLGVHEFKEGKDEISEQ 120
QY      121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP 180
Db      121 DEMFRGRTAVFADQVIVGNASRLKNVQLTDAGTYKCYITTSKGNANLEYKTGAFSMP 180
QY      181 EVNVVDYNASSELRCEAPRPFQPTVWASQVDQANFSEVSNTSFEINSENVTKVSV 240
Db      181 EVNVVDYNASSELRCEAPRPFQPTVWASQVDQANFSEVSNTSFEINSENVTKVSV 240
QY      241 LYNVTINNNTSCMIENDIAKATGDIKVTSEIKRSHLOLNSKASLCVSSFFAISWALL 300
Db      241 LYNVTINNNTSCMIENDIAKATGDIKVTSEIKRSHLOLNSKASLCVSSFFAISWALL 300
QY      301 PLSPYIMLK 309
Db      301 PLSPYIMLK 309
```

## RESULT 4

```
US-09-907-969-392
; Sequence 392, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Hill, Paul
; APPLICANT: Albane, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; NUMBER OF SEQ ID NOS: 2001-07-17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 392
; LENGTH: 309
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-907-969-392

Query Match      100.0%; Score 1574; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60
   1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60
Db 1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60

QY 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120
   61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120
Db 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120

QY 121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180
   121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180
Db 121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180

QY 181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240
   181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240
Db 181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240

QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300
   241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300
Db 241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300

QY 301 PLSPLYMLK 309
   301 PLSPLYMLK 309
Db 301 PLSPLYMLK 309

RESULT 5
US-09-827-271-392
; Sequence 392, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827, 271
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 392
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-392

Query Match      100.0%; Score 1574; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60
   1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60
Db 1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60

QY 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120
   61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120
Db 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120

QY 121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180
   121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180
Db 121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180

QY 181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240
   181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240
Db 181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240

QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300
   241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300
```

```
Db 241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300

QY 301 PLSPLYMLK 309
   301 PLSPLYMLK 309
Db 301 PLSPLYMLK 309

RESULT 6
US-10-010-742-209
; Sequence 209, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuguin
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010, 742
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 209
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-742-209

Query Match      100.0%; Score 1574; DB 13; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60
   1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60
Db 1 HASAHASGRQRLHSASTQIRWPPSPAMASLGQILFWSIIISIIIIAGATAIILIGFISG 60

QY 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120
   61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120
Db 61 RHSITVTVASAGNIGEDGILSCTFEEDIKLSDIVIOWLKEGVLGVHEFEKGDELSEQ 120

QY 121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180
   121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180
Db 121 DEMFRGRTAVFADQVIVGNASIRLKNVQLTDAGTYKCYIITSKGNANLEYKTGAFSMP 180

QY 181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240
   181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240
Db 181 EVANVDYNASSETLRCEAPRWFPOPTVWVASQVDQGANFSEVSNTSEFELNSENVTMKVSV 240

QY 241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300
   241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300
Db 241 LYNVTINNNTYSCMIENDIAKATGDIKVTESIKRSHLQLNSKASLGVSSFFAISWALL 300

QY 301 PLSPLYMLK 309
   301 PLSPLYMLK 309
Db 301 PLSPLYMLK 309

RESULT 7
US-10-198-053-392
; Sequence 392, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
```

```
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-198-053-392

Query Match      100.0%; Score 1574; DB 14; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.5e-138;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HASAHASGRORLHASASTQIRWEPSPAMASLGQILFWSIISIIIIILAGALIIIGFISG 60
DB 1 HASAHASGRORLHASASTQIRWEPSPAMASLGQILFWSIISIIIIILAGALIIIGFISG 60
QY 61 RHSTVTTVASAGNIGEDGILSCTFEEDIKLSDIVIQLMKEGVLGVHEFEKDELSEQ 120
DB 61 RHSTVTTVASAGNIGEDGILSCTFEEDIKLSDIVIQLMKEGVLGVHEFEKDELSEQ 120
QY 121 DEMFRGRTAVFADQIVYGNASLRLKNVQLTDAGTYKCYIITSKGNANLEYKTAFAFSP 180
DB 121 DEMFRGRTAVFADQIVYGNASLRLKNVQLTDAGTYKCYIITSKGNANLEYKTAFAFSP 180
QY 181 EVNVDMASSETLRCEAPRFPQPTVVASQVDGAFSEVSNSEFELSENVTMKVSV 240
DB 181 EVNVDMASSETLRCEAPRFPQPTVVASQVDGAFSEVSNSEFELSENVTMKVSV 240
QY 241 LYNTVINTYSCMIENDIAKATGDIKYTESEIKRSHQLNLSKASLCVSSFFATSWALL 300
DB 241 LYNTVINTYSCMIENDIAKATGDIKYTESEIKRSHQLNLSKASLCVSSFFATSWALL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309
```

```
RESULT 8
US-09-778-320-208
Sequence 208, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 208
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
US-09-778-320-208
```

```
Query Match      90.9%; Score 1431; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 28 MASIGQILFWSIISIIIIILAGALIIIGFISGRHSITVTT
DB 1 MASIGQILFWSIISIIIIILAGALIIIGFISGRHSITVTT
QY 88 DIKLSDIVIQLMKEGVLGVHEFEKDELSEODEMFRGRTA
DB 61 DIKLSDIVIQLMKEGVLGVHEFEKDELSEODEMFRGRTA
QY 148 QLTDACTYKCYIITSKGNANLEYKTAFAFSPENVVDYNASSE
DB 121 QLTDACTYKCYIITSKGNANLEYKTAFAFSPENVVDYNASSE
QY 208 MASQVDGAFSEVSNSEFELSENVTMKVSVLYNTVINTYSCMIENDIAKATGDIK 267
DB 181 MASQVDGAFSEVSNSEFELSENVTMKVSVLYNTVINTYSCMIENDIAKATGDIK 240
QY 268 TSESEIKRSHQLNLSKASLCVSSFFATSWALLPLSPYMLK 309
DB 241 TSESEIKRSHQLNLSKASLCVSSFFATSWALLPLSPYMLK 282
```

```
RESULT 9
US-09-850-178-33
Sequence 33, Application US/09850178
Patent No. US20020034749A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Russell, John C.
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Stroupe, Stephen D.
APPLICANT: Gordon, Julian
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
FILE REFERENCE: 6251.US.P1
CURRENT APPLICATION NUMBER: US/09/850,178
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 08/972,376
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-178-33
```

```
Query Match      90.9%; Score 1431; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.1e-124;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 28 MASIGQILFWSIISIIIIILAGALIIIGFISGRHSITVTTVASAGNIGEDGILSCTFE 87
DB 1 MASIGQILFWSIISIIIIILAGALIIIGFISGRHSITVTVASAGNIGEDGILSCTFE 60
QY 88 DIKLSDIVIQLMKEGVLGVHEFEKDELSEODEMFRGRTAVFADQIVGNASLRLKNV 147
DB 61 DIKLSDIVIQLMKEGVLGVHEFEKDELSEODEMFRGRTAVFADQIVGNASLRLKNV 120
QY 148 QLTDACTYKCYIITSKGNANLEYKTAFAFSPENVVDYNASSETLRCEAPRFPQPTVV 207
DB 121 QLTDACTYKCYIITSKGNANLEYKTAFAFSPENVVDYNASSETLRCEAPRFPQPTVV 180
QY 208 WASQVDGAFSEVSNSEFELSENVTMKVSVLYNTVINTYSCMIENDIAKATGDIK 267
```



PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 90.9%; Score 1431; DB 9; Length 282;  
Best Local Similarity 100.0%; Pred. No. 1,1e-124;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 WASQVQGANFSEVSNSTSEFENSEVNTKRVSVLYNVTINNTYSCMIENDIAKATGDIKY 240  
QY 268 TESEIKRRSHLQILNSKASLCVSSFFAISWALLPLSPYMLK 309  
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; Sequence 291, Application US/09989723  
; Patent No. US20020072092A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Inc

APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C62  
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46 PRIOR APPLICATION NUMBER: 60/092182
47 PRIOR FILING DATE: 1998-07-09

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Query Match	90.9%	Score 1431	DB 9	Length 282
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Db	61	DILSLDIYIOWLKEGVGLGVHFEKKGKDELSEQDEMFRGRTAVADQYIVGNASRLKNV	120	
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QY	268	TSESEIKRRSHLOLNSKASLVCVSSFPATSWALLPLSPYIMLK	309	
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RESULT 13
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/ Patent No. US20020072496A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Denoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gottlieb, Mary E.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
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/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C56
/ CURRENT APPLICATION NUMBER: US/09/989,279
/ CURRENT FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 60/049787
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/ Patent No. US20020081609A1
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/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Jiang, Yuguu
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Mitcham, Jennifer
/ APPLICANT: Wang, Tongtong
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Harlocker, Susan L.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.491C6
/ CURRENT APPLICATION NUMBER: US/09/910.689
/ NUMBER OF SEQ ID NOS: 307
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 208
/ LENGTH: 282
/ TYPE: PRT
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